

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
944	1hle	A	175	498	7e-99			132.76	HYDROLASE INHIBITOR/SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLE) 1HLE 3	
944	1l89	I	168	532	1.5e-64			167.27	ALASERPIN; CHAIN: I; TRYPSIN II, ANIONIC; CHAIN: E; 3	HYDROLASE/HYDROLASE INHIBITOR SERPIN I; PRETRYPSINOGEN II; MICHAELIS SERPIN-PROTEASE COMPLEX INHIBITORY TRIAD
944	1l89	I	6	370	7e-81			169.22	ALASERPIN; CHAIN: I; TRYPSIN II, ANIONIC; CHAIN: E;	HYDROLASE/HYDROLASE INHIBITOR SERPIN I; PRETRYPSINOGEN II; MICHAELIS SERPIN-PROTEASE COMPLEX INHIBITORY TRIAD
944	1ov8	A	12	370	2.8e-94			151.89	SERPIN OVALBUMIN (BOG ALBUMIN) IOVA 3	
944	1ov8	A	174	532	1.4e-96			151.52	SERPIN OVALBUMIN (BOG ALBUMIN) IOVA 3	
944	1ov8	A	176	532	1.4e-96	0.53	1.00		SERPIN OVALBUMIN (BOG ALBUMIN) IOVA 3	
944	1alp	A	12	372	0			171.59	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1- ANTITRYPSINASE: SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE

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SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
944	1qjp	A	174	534	0			170.59	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE, SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
944	1qjp	A	175	532	0	0.46	1.00		ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE, SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
944	1qmb	B	502	532	9.8e-09	-0.75	0.05		ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-P1, SERPIN, ANTITRYPSIN, POLYMER, CLEAVED
944	1qmn	A	14	372	0			184.90	ALPHA-1-ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
944	1qmn	A	176	533	0	0.46	1.00		ALPHA-1-ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION,

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944	1qmm	A	176	534	0			183.22	ALPHA-1- ANTICENTROTYPIN; CHAIN: A;	EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
944	1aek		168	532	1.4e-81			143.79	SERPIN K; CHAIN: NULL;	SERINE PROTEASE INHIBITOR, SERINE PROTEASE INHIBITOR, SERPIN, PROTEASE
944	1aek		6	370	2.8e-80			145.58	SERPIN K; CHAIN: NULL;	SERINE PROTEASE INHIBITOR, SERINE PROTEASE INHIBITOR, SERPIN, PROTEASE
945	1f2l	A	80	188	4.2e-25	0.40	1.00		PROTEIN ARGININE METHYLTRANSFERASE PRMT3; CHAIN: A;	TRANSFERASE BETA BARREL, ROSSMANN FOLD, ARGININE METHYLTRANSFERASE
945	1f2l	A	80	213	1.7e-05	-0.30	0.23		PROTEIN ARGININE METHYLTRANSFERASE PRMT3; CHAIN: A;	TRANSFERASE BETA BARREL, ROSSMANN FOLD, ARGININE METHYLTRANSFERASE
945	1g6q	1	81	219	1.4e-25	0.03	0.57		HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
947	1av1	A	1	193	2.8e-09			56.50	ATPOLYPROTEIN A-1; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-1; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT- ACTIVATION
947	1c1g	A	13	296	1.3e-29			96.22	TROPOMYOSIN; CHAIN:	CONTRACTILE PROTEIN

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SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pat Blast	Verify score	PMF score	SEQ/PROL D score	Compound	PDB annotation
									A, B, C, D	TROPOMYOSIN COILED-COIL, ALPHA-HELICAL, CONTRACTILE PROTEIN
947	1c1g	A	249	532	4.2e-28			105.38	TROPOMYOSIN, CHAIN: A, B, C, D	CONTRACTILE PROTEIN, TROPOMYOSIN COILED-COIL, ALPHA-HELICAL, CONTRACTILE PROTEIN
947	1eun	A	190	417	1.7e-13	0.09	-0.05		ALPHA SPECTRIN, CHAIN: A, B, C	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
947	1eun	A	249	504	3.4e-19	0.11	0.52		ALPHA SPECTRIN, CHAIN: A, B, C	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
947	1eun	A	412	536	6.8e-08	0.05	0.03		ALPHA SPECTRIN, CHAIN: A, B, C	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
947	1eun	A	4	206	0.0097			56.15	ALPHA SPECTRIN, CHAIN: A, B, C	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
947	1eun	A	55	271	0.00011			69.05	ALPHA SPECTRIN, CHAIN: A, B, C	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
947	1dnl	B	1	190	0.0025			55.90	SYNTAXIN BINDING PROTEIN 1, CHAIN: A	ENDOCYTOSIS/EXOCYTOSIS NSBC1, PROTEIN-PROTEIN



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947	1dnl	B	366	527	1.2e-12	0.13	-0.15		SYNTAXIN 1A; CHAIN: B;	COMPLEX, MULTI-SUBUNIT
									SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSBC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
947	1dnl	B	53	284	0.0066			63.83	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSBC; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
947	1dnp	A	475	575	3.4e-20	-0.06	0.28		HEPATOCYTE GROWTH FACTOR-REGULATED TYROSINE CHAIN: A; SSOI PROTEIN; CHAIN: A;	TRANSFERRASE HRS; HRS, VHS, FYVE, ZINC FINGER, SUPERHELIX
947	1fio	A	2	191	0.0097			62.09	MEMBRANE PROTEIN FOUR HELIX BUNDLE ALPHA HELIX	
947	1lci	A	126	570	1.7e-30			114.13	ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN-BINDING PROTEIN
947	1lci	A	188	553	1.7e-29	-0.13	0.22		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN-BINDING PROTEIN
947	1lci	A	189	511	1.7e-30	-0.15	0.10		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN,

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SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQPOL ID score	Compound	PDB annotation
947	1byf	A	531	580	5.1e-19	0.11	0.75		ENDOSOME-ASSOCIATED PROTEIN; CHAIN: A;	MUSCLE, 2,2-LINK, ACTIN-BINDING PROTEIN
947	1byf	A	5	68	1.1e-19			62.30	ENDOSOME-ASSOCIATED PROTEIN; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SHEET, ALPHA HELIX, ZINC CLUSTER, PTDINS3P
947	1byf	A	5	68	1.1e-19				ENDOSOME-ASSOCIATED PROTEIN; CHAIN: A;	BETA SHEET, ALPHA HELIX, ZINC CLUSTER, PTDINS3P
947	1quu	A	297	517	1.7e-18	0.11	-0.15		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, PROTEIN
947	1vy	A	531	575	6.8e-16	-0.08	0.69		PHOSPHATIDYLINOSITOL-3-PHOSPHATE BINDING FYVE CHAIN: A;	TRANSPORT PROTEIN FYVE DOMAIN, ENDOSOME MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN
947	1zbd	B	496	603	6.8e-23	0.02	-0.02		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDN, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
950	1bee		111	237	5.6e-26			94.09	CD94; CHAIN: NULL;	NK CELL, NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
950	1bee		1	118	7e-25			76.63	CD94; CHAIN: NULL;	NK CELL, NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
950	1bj3	A	112	233	2.8e-36	0.21	0.69		COAGULATION FACTOR IX-BINDING PROTEIN A; COAGULATION FACTOR	COIL-LEGEN BINDING PROTEIN IX-BP, IX-BP, COAGULATION FACTOR IX-BINDING, HETERODIMER, VERNOM, HABU 2

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950	1b03	A	112	234	2.8e-36			66.57	IX-BINDING PROTEIN B; CHAIN: B;	SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
950	1b03	A	112	234	2.8e-36			66.57	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A;	COLLAGEN BINDING PROTEIN IX-BP: IX-BP: COAGULATION FACTOR IX-BINDING HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
950	1c3a	B	110	236	1.4e-35			68.42	FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
950	1c3a	B	112	236	1.4e-35	0.48	1.00		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
950	1c3a	B	1	117	1.3e-30			50.64	FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
950	1d48	A	113	233	1.4e-32	0.63	1.00		ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HERPATIC LECTIN IH; C-TYPE LECTIN CRD
950	1d48	A	113	241	1.4e-32			69.21	ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HERPATIC LECTIN IH; C-TYPE LECTIN CRD
950	1e87	A	111	236	5.6e-27			81.55	EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE (AIM), EA 1, RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE 2 NKD KLR
950	1e87	A	1	117	1.1e-24			60.58	EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR ACTIVATION

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									A;	INDUCER MOLECULE (AUM), EA 1, HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NMD, KLR
950	1egg	A	113	236	4.2e-28			53.59	MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
950	1egg	B	110	241	7e-29			60.69	MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
950	1fpu	A	112	237	4.2e-30			52.01	BOTROCETIN ALPHA CHAIN; CHAIN: A, C; BOTROCETIN BETA CHAIN; CHAIN: B, D;	TOXIN PLATELET COAGULUTININ ALPHA; PLATELET COAGULUTININ BETA VON WILLEBRAND FACTOR MODULATOR, C-TYPE LECTIN, METAL-2 BINDING, LOOP EXCHANGED DIMER
950	1fpu	B	112	236	4.2e-34	0.58	0.99		BOTROCETIN ALPHA CHAIN; CHAIN: A, C; BOTROCETIN BETA CHAIN; CHAIN: B, D;	TOXIN PLATELET COAGULUTININ ALPHA; PLATELET COAGULUTININ BETA VON WILLEBRAND FACTOR MODULATOR, C-TYPE LECTIN, METAL-2 BINDING, LOOP EXCHANGED DIMER
950	1fpu	B	112	236	4.2e-34			69.59	BOTROCETIN ALPHA CHAIN; CHAIN: A, C; BOTROCETIN BETA CHAIN; CHAIN: B, D;	TOXIN PLATELET COAGULUTININ ALPHA; PLATELET COAGULUTININ BETA VON WILLEBRAND FACTOR MODULATOR, C-TYPE LECTIN, METAL-2 BINDING, LOOP EXCHANGED DIMER
950	1fpu	B	1	117	1.4e-28			50.65	BOTROCETIN ALPHA CHAIN; CHAIN: A, C; BOTROCETIN BETA CHAIN; CHAIN: B, D;	TOXIN PLATELET COAGULUTININ ALPHA; PLATELET COAGULUTININ BETA VON WILLEBRAND FACTOR

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										MODULATOR, C-TYPE LECTIN, METAL-2 BINDING, LOOP EXCHANGED DIMER
950	1hg8	A	108	237	4.2e-30			93.99	NIK2-D; CHAIN: A;	APOPTOSIS HOMODIMER, CIS-PROLINE
950	1hg8	A	1	118	2.8e-28			66.38	NIK2-D; CHAIN: A;	APOPTOSIS HOMODIMER, CIS-PROLINE
950	1hyr	A	107	237	4.2e-28			92.55	NIK2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B; A; MHC CLASS I CHAIN-RELATED PROTEIN A;	IMMUNE SYSTEM NEK2D; MHC-A, MIC, PERB1; ACTIVATING NK CELL RECEPTOR, NEK2D, C-TYPE LECTIN LIKE, MIC-2 A, MHC-1 COMPLEX, IMMUNE SYSTEM
950	1hyr	A	1	118	5.6e-24			65.31	NIK2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B; A; MHC CLASS I CHAIN-RELATED PROTEIN A;	IMMUNE SYSTEM NEK2D; MHC-A, MIC, PERB1; ACTIVATING NK CELL RECEPTOR, NEK2D, C-TYPE LECTIN LIKE, MIC-2 A, MHC-1 COMPLEX, IMMUNE SYSTEM
950	1lod	A	112	233	1.3e-33	0.13	0.82		COAGULATION FACTOR X BINDING PROTEIN;	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING
									COAGULATION FACTOR X BINDING PROTEIN;	
									COAGULATION FACTOR X BINDING PROTEIN;	
									COAGULATION FACTOR X GLA DOMAIN; CHAIN: G;	
950	1lod	A	112	234	1.3e-33			59.17	COAGULATION FACTOR X BINDING PROTEIN;	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING

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SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PAIR score	SEQPOL ID score	Compound	PDB annotation
950	1lod	B	112	236	9.8e-36	0.56	1.00		X GLA DOMAIN; CHAIN: G;	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING
950	1lod	B	112	236	9.8e-36			60.25	COAGULATION FACTOR X BINDING PROTEIN; CHAIN: A; COAGULATION FACTOR X BINDING PROTEIN; CHAIN: B; COAGULATION FACTOR X GLA DOMAIN; CHAIN: G;	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING
950	1lxx	A	112	233	7e-34	0.19	0.76		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
950	1lxx	A	112	234	7e-34			62.61	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
950	1lxx	B	112	236	9.8e-36	0.48	1.00		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER

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SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pst Blast	Verify score	PMR score	SEQPOL D score	Compound	PDB annotation
950	1lxx	B	112	236	9.8e-36			65.36	C, D, E, F; COAGULATION FACTORS IX-X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F; DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER	DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
950	1lht		113	235	4.2e-35	0.65	1.00		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, LECTIN
950	1lht		113	241	4.2e-35			59.42	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, LECTIN
950	1lht		1	122	1.3e-28			52.81	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, LECTIN
950	1qdd	A	101	235	9.8e-36	0.52	1.00		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN, PANCREATIC STONE PROTEIN, PSP, PANCREATIC STONE INHIBITOR, LITHOSTATHINE
950	1qdd	A	101	241	9.8e-36			64.36	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN, PANCREATIC STONE PROTEIN, PSP, PANCREATIC STONE INHIBITOR, LITHOSTATHINE
950	1qg3	C	105	236	6.8e-27			72.18	MHC CLASS I H-2DQ HEAVY CHAIN; CHAIN: A: BETA-2- MICROGLOBULIN; CHAIN: B: HIV ENVELOPE GLYCOPROTEIN 120 PERTIDE; CHAIN: P;	CLASS I H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M, NK-CELL SURFACE GLYCOPROTEIN YE146, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M,

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950	1qg3	C	1	117	4.2<25			52.76	LY49A; CHAIN: C, D; MHC CLASS I H-2D HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	LY49, LY-49 COMPLEX (NK RECEPTOR/MHC CLASS II H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN 148, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
950	1qg3	D	115	238	7<26			65.45	MHC CLASS I H-2D HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS II H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN 148, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
950	1qg3	D	1	119	4.2<25			56.68	MHC CLASS I H-2D HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS II H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN 148, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
950	1m3		108	238	2.8<28			50.25	LECTIN XEIRANECTIN; NULL;	LECTIN XEIRANECTIN; PLASINIOGEN BINDING; KRINGLE 4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN
950	2a1p	A	107	241	2.8<29			63.07	SEA RAVEN TYPE II ANTITRIBES PROTEIN;	ANTITRIBES PROTEIN RECOGNIZANT SEA RAVEN



Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PAM score	SEQPOL D score	Compound	PDB annotation
									CHAIN: A;	PROTEIN SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIREZEZ PROTEIN
951	1b13	A	198	280	4.2e-26	0.10	0.09		COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A;	COLLAGEN BINDING PROTEIN IX-BP-IX-BP: COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
951	1c3a	B	197	281	4.2e-27	0.10	0.39		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
951	1d48	A	198	276	1.4e-24	0.22	0.68		ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A; BOTROCETIN ALPHA CHAIN; CHAIN: A; C; BOTROCETIN BETA CHAIN; CHAIN: B; D;	SIGNALING PROTEIN HEPATIC LECTIN HI, C-TYPE LECTIN CRD TOXIN PLATELET COAGULITIN ALPHA; VON WILLEBRAND FACTOR MODULATOR, C-TYPE LECTIN, METAL-2 BINDING, LOOP EXCHANGED DIMER
951	1f7u	B	198	280	1.4e-26	0.07	0.47			
951	1hg8	A	193	280	8.4e-28	0.17	0.58		NKG2-D; CHAIN: A;	PROLINE APOPTOSIS HOMODIMER, CIS-PROLINE
951	1hyr	A	192	279	1.4e-25	-0.08	0.90		NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B; A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D, MIC-A, MIC, PERB1; ACTIVATING NK CELL RECEPTOR, NKG2D, C-TYPE LECTIN LIKE, MIC-2 A, MHC-1 COMPLEX, IMMUNE SYSTEM
951	1lcl	A	198	280	7e-25	0.02	0.19		COAGULATION FACTOR X-BINDING PROTEIN; CHAIN: A;	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PAM score	SEQPOL D score	Compound	PDB annotation
951	1lod	B	198	280	2.8e-25	-0.02	0.01		COAGULATION FACTOR X BINDING PROTEIN; CHAIN: B; COAGULATION FACTOR X GLA DOMAIN; CHAIN: G;	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING
951	1lxx	B	198	281	4.2e-26	-0.12	0.09		COAGULATION FACTORS IX-X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX-X-BP COAGULATION FACTOR BINDING C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF LOOP EXCHANGED DIMER
951	2a2p	A	193	281	1.4e-24	0.38	0.46		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN POLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN TRANSFERASE ALPHA-BETA STRUCTURE
952	1g9r	A	1242	1507	1e-44	0.19	0.93		GLYCOSYL TRANSFERASE; CHAIN: A;	HYDROLASE TETRAHYDROPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TRP, 2 SUPER-HHLLX, X-RAY STRUCTURE
953	1a17		68	229	2.8e-16	0.33	1.00		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMR score	SEQPOL D score	Compound	PDB annotation
953	1etf	A	152	227	0.00014	0.14	0.60		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEVD, CHAIN: B	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
953	1etf	A	65	218	1e-09	0.22	0.99		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEVD, CHAIN: B	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
953	1etw	A	65	217	1.7e-13	0.47	0.81		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
953	1etw	A	68	215	1.3e-08	0.44	0.95		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
953	1etw	A	71	226	3.4e-09	0.20	0.62		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A; B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP, PEROXIN5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPETIDE REPEAT, TPR, 2 HELICAL REPEAT
953	1hh8	A	150	198	2.8e-05	0.06	0.43		NEUTROPHIL CYTOSOL FACTOR 2; CHAIN: A	PHAGOCYTE OXIDASE FACTOR P67PHOX, NCF-2, PHAGOCYTE OXIDASE FACTOR, SH DOMAIN, REPEAT, TPR REPEAT
953	1hhg	A	68	226	8.4e-37	0.39	1.00		CYCLOPHILIN 40; CHAIN: A	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; TETRATRICOPETIDE
957	1htf		1	203	5.6e-32	-0.35	0.18		FIBRONECTIN, IYFN 6 CHAIN: NULG, IYFN-7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IYFN 18
957	1htb	A	1	192	1.3e-27	-0.20	0.11		FIBRONECTIN, CHAIN:	HEPARIN AND INTEGRIN

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	Seq/OL ID score	Compound	PDB annotation
									A;	BINDING HEPARIN AND INTEGRIN BINDING
957	1fth	A	31	201	2.8e-22	-0.22	0.27		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
957	1lfr	A	29	202	1.3e-12	0.14	-0.19		INTERLEUKIN-6 RECEPTOR BETA CHAIN; CHAIN: A; VIRAL IL-6; CHAIN: B;	CYTOKINE GP130; FUNCTIONAL INTERLEUKIN-6 HOMOLOG; CYTOKINERECEPTOR COMPLEX; GP130; VIRAL IL-6; CRYSTAL 2 STRUCTURE
957	1mth		29	204	4.2e-29			66.80	FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
957	1mth		2	112	1.4e-23	0.12	-0.08		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
957	1mth		31	203	4.2e-29	0.11	0.41		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
957	1qg3	A	29	194	4.2e-24			57.81	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	INTEGRIN, HEMIDESMOsome, FIBRONECTIN, CARCINOMA, STRICKTURAL 2 PROTEIN
957	1qf4	A	31	204	2.8e-21			71.24	TENASCIN; CHAIN: A, B;	TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQIDOL D score	Compound	PDB annotation
957	1qr4	A	33	193	2.8e-21	0.01	0.27		TENASCIN CHAIN: A, B	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
957	1qr4	A	3	117	7e-20	-0.25	0.84		TENASCIN CHAIN: A, B	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
957	1ten		11	98	8.4e-16			53.41	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) ITEN 3	
957	1ten		30	117	1.7e-18			53.70	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) ITEN 3	
957	1ttf		11	99	4.2e-21			51.26	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMAR, 36 STRUCTURES) ITTF 3	
957	1ttf		30	121	8.4e-18			51.78	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMAR, 36 STRUCTURES) ITTF 3	
958	1qge		123	282	5.6e-71	1.17	1.00		HYDROLASE (METALLOPROTEASE) COLLAGENASE (EC 3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM 1 CGE 3	

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
958	1cgc		123	283	5.1e-74			280.54	HYDROLASE (METALLOPROTEASE) COLLAGENASE (EC 3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I CGE	
958	1cgc		123	284	5.1e-74	1.12	1.00		3 HYDROLASE (METALLOPROTEASE) COLLAGENASE (EC 3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I CGE	
958	1cgc		76	188	4.2e-55			176.37	3 HYDROLASE (METALLOPROTEASE) COLLAGENASE (EC 3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I CGE	
958	1ck7	A	27	246	4.2e-73	0.27	0.99		3 GELATINASE A; CHAIN: A;	HYDROLASE MMP-2/72KD TYPE IV COLLAGENASE, HYDROLASE (METALLOPROTEASE), FULL-LENGTH, METALLOPROTEINASE, 2 GELATINASE A
958	1bl		121	487	0	1.03	1.00		FIBROBLAST (INTERSTITIAL) COLLAGENASE (MMP-13) IPBL 4 CHAIN: NULL; IPBL 5	METALLOPROTEASE
958	1bl		121	487	0			592.38	FIBROBLAST (INTERSTITIAL) COLLAGENASE (MMP-13) IPBL 4 CHAIN: NULL;	METALLOPROTEASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pos Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
958	1b6l		74	188	7e-58			57.48	1HBL 5 FIBROBLAST (INTERSTITIAL) COLLAGENASE (NMP-1) 1HBL 4 CHAIN: NULL; 1HBL 5	METALLOPROTEINASE
958	1b6c		128	282	1.4e-70	1.08	1.00		METALLOPROTEINASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) HIFC 3	
958	1b6c		128	284	1.4e-70			274.25	METALLOPROTEINASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) HIFC 3	
958	1b6c		81	188	5.6e-55			168.69	METALLOPROTEINASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) HIFC 3	
958	1lbu		50	127	0.0014	0.42	0.24		MURAMYL- PENTAPEPTIDE CARBOXYPEPTIDASE; CHAIN: NULL;	HYDROLASE HYDROLASE, NUCLEAR RECEPTOR, CARBOXYPEPTIDASE
958	1s8t		47	490	1.4e-34			78.13	SERRATIN PROTEINASE ISAT 3	HYDROLASE (SERINE PROTEINASE) SERRATIN, MAJOR METALLO PROTEINASE FROM ISAT 4 PARALLEL BETA HELIX, PARALLEL BETA ROLL ISAT 7
958	1s8t		83	406	1.4e-34	0.21	0.39		SERRATIN PROTEINASE ISAT 3	HYDROLASE (SERINE PROTEINASE) SERRATIN, MAJOR METALLO PROTEINASE FROM ISAT 4 PARALLEL BETA HELIX, PARALLEL BETA ROLL ISAT 7
958	1s8m		54	285	1.1e-96	0.76	1.00		STROMELYSIN-1; CHAIN: NULL;	HYDROLASE MATRIX METALLOPROTEINASE-3;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMR score	SEQ ID score	Compound	PDB annotation
										PROTEOGLYCANASE; HYDROLASE; METALLOPROTEINASE; FIBROBLAST, COLLAGEN DEGRADATION
958	1alm		55	285	1.1e-96			271.16	STROMELYSIN-1; CHAIN: NULL;	HYDROLASE MATRIX METALLOPROTEINASE-3; PROTEOGLYCANASE; HYDROLASE; METALLOPROTEINASE; FIBROBLAST, COLLAGEN DEGRADATION
958	1alm		8	187	2.8e-83			190.20	STROMELYSIN-1; CHAIN: NULL;	HYDROLASE MATRIX METALLOPROTEINASE-3; PROTEOGLYCANASE; HYDROLASE; METALLOPROTEINASE; FIBROBLAST, COLLAGEN DEGRADATION
962	1ap0		35	106	3e-14			50.89	MODIFIER PROTEIN I; CHAIN: NULL;	CEROMATIN-BINDING MODIFI, HETEROCHROMATIN PROTEIN I; CEROMATIN-BINDING, PROTEIN INTERACTION MOTIF, ALPHA+BETA
964	1abq	L	20	242	8.4e-66			110.96	29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE
964	1a2y	A	1	101	9.8e-39			51.49	MONOCLONAL ANTIBODY D1.3; CHAIN: A, B: LYSOZYME; CHAIN: C;	COMPLEX (MUNOGLILOBULIN/HYDROLAS B) COMPLEX (MUNOGLILOBULIN/HYDROLAS B), IMMUNOGLOBULIN V2 REGION, SIGNAL, HYDROLASE, GLYCOSIDASE, BACTERIOLYTIC 3 ENZYME, EGG WHITE



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pst Blast	Verify score	PMR score	SEQ/ROL D score	Compound	PDB annotation
964	1a7q	L	1	101	4.2e-37			53.02	MONOCLONAL ANTIBODY DJ.3; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, VARIANT
964	1adq	L	21	246	8.4e-72			111.15	IGG4 REA; CHAIN: A, RF- ANIGLAMBD4; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN). REHUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
964	1ae6	L	19	243	2.8e-65			107.14	ANTIBODY CTM01; CHAIN: L, H;	IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
964	1afv	H	24	239	5.6e-85	0.22	-1202.08		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV- 1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
964	1ahw	A	19	243	2.8e-71			109.26	IMMUNOGLOBULIN FAB 509; CHAIN: A, B, D, E; TISSUE FACTOR; CHAIN: C, F;	COMPLEX (IMMUNOGLOBULIN/TISSUE FACTOR) FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN, TF, THROMBOPLASTIN, COAGULATION FACTOR III; BLOOD COAGULATION, TISSUE FACTOR, FAB, COMPLEX, ANTIBODY, 2 COMPLEX (IMMUNOGLOBULIN/TISSUE FACTOR)
964	1aif	A	19	245	5.6e-69			107.73	ANTI-IDIOTYPE FAB 409.5.3 (GGGA) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
964	1aek	L	21	246	2.8e-68			110.74	FAB B7-15A2; CHAIN: L, H;	IMMUNOGLOBULIN HUMAN FAB, ANTI-LETTANUS TOXOID, HIGH

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	D score	Compound	PDB annotation
										AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING PROPENSITY TO CRYSTALLIZE, 3
964	1ey1	L	19	238	76-72			111.56	TP7 FAB; CHAIN: L, H;	IMMUNOGLOBULIN
964	1b0w	A	1	101	42-45			50.86	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C;	IMMUNOGLOBULIN, ANTIBODY, FAB, ENZYME INHIBITOR, PCK, 2 HOT START
964	1bat	L	19	243	146-71			107.96	IMMUNOGLOBULIN FAB FRAGMENT OF MURINE MONOCLONAL ANTIBODY AN02 COMPLEX IBAF 3 WITH ITS HAFTEN (2,2,6,6-TETRAMETHYL-1,1-PHOSPHONATOXY-1BAF 4 DINITROPHENYL)	IMMUNE SYSTEM
964	1bj1	J	19	242	286-74			107.19	FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
964	1bjm	A	20	246	146-66			115.09	LOC-14MBDA 1 TYPE LIGHT-CHAIN DIMER; IBAF 6 CHAIN: A, B; IBAF 7	IMMUNOGLOBULIN BENCE-JONES PROTEIN; IBAF 8 BENCE JONES ANTIBODY; MULTIPLE QUATERNARY STRUCTURES IBAF 13
964	1bvk	A	1	101	116-44			52.15	HULYSII; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
964	1hw <sup>w</sup>	A	1	101	4.2e-47			50.82	IG KAPPA CHAIN V-L REGION REI; CHAIN: A, B;	ANTIBODY, ANTIBODY COMPLEX, PV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED) ANTIBODY/HYDROLASE
964	1e1g	A	1	234	8.4e-43			63.76	TROPOMYOSIN; CHAIN: A, B, C, D	IMMUNE SYSTEM REIN, STABILIZED IMMUNOGLOBULIN FRAGMENT, RENCE-JONES 2 PROTEIN, IMMUNE SYSTEM CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
964	1d5l	L	19	238	9.8e-69			108.44	CHIMERIC GERMALINE PRECURSOR OF OXY-COPE CHAIN: L; CHIMERIC GERMALINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNE SYSTEM IMMUNE SYSTEM
964	1e4k	H	24	238	1.3e-81	0.14	-1202.08		TAB2; CHAIN: L, M; TAB2; CHAIN: H, L; CYCLIC PEPTIDE; CHAIN: P, Q	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN-PEPTIDE RECOGNITION
964	1e6o	H	24	239	5.6e-82	0.22	-1202.08		IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H;	IMMUNOGLOBULIN FAB, ANTIBODY, ANTIGEN, HIV-1, P24, CA
964	1f8t	L	19	243	2.8e-65			107.82	ANTIBODY FAB FRAGMENT (LIGHT CHAIN); CHAIN: L; ANTIBODY FAB FRAGMENT (HEAVY CHAIN); CHAIN: H	IMMUNE SYSTEM MONOCLONAL ANTIBODY, ANTIGEN-BINDING FRAGMENT, INTERLEUKIN-2, X-RAY ANALYSIS, CRYSTAL
964	1f8t	H	24	239	2.8e-81	0.07	-1202.08		COMPLEX	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL ID score	Compound	PDB annotation
964	1fgn	H	24	238	2.8e-83	0.25	-1202.08		(ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE MONOCLONAL ANTIBODY F9.13.7 (IGG1) IBB 3 COMPLEXED WITH LYSOZYME (EC3.2.1.17) IBB 4	
964	1fgn	H	24	238	2.8e-83	0.25	-1202.08		IMMUNOGLOBULIN FAB 509; CHAIN: L, H	IMMUNOGLOBULIN FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN; ANTIBODY, FAB, ANTI-TF, MONOCLONAL, MURINE, IMMUNOGLOBULIN
964	1q1	A	19	242	5.6e-68			113.25	HYBRIDOMA ANTIBODY LA2 (LIGHT CHAIN); CHAIN: A, C; HYBRIDOMA ANTIBODY LA2 (HEAVY CHAIN); CHAIN: B, D; OUTER SURFACE PROTEIN A; CHAIN: E, F; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A; IGG2A, KAPPA ANTIBODY CB41 (HEAVY CHAIN); CHAIN: B; PEPTIDE 5; CHAIN: C;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A, ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN, BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY CROSSREACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1
964	1hs	L	19	243	9.8e-71			107.73	IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A; IGG2A, KAPPA ANTIBODY CB41 (LIGHT CHAIN); CHAIN: A; IGG2A, KAPPA ANTIBODY CB41 (HEAVY CHAIN); CHAIN: B; PEPTIDE 5; CHAIN: C;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A, ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN, BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY CROSSREACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1
964	1hi6	A	19	243	1.3e-66			109.95	IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A; IGG2A, KAPPA ANTIBODY CB41 (LIGHT CHAIN); CHAIN: A; IGG2A, KAPPA ANTIBODY CB41 (HEAVY CHAIN); CHAIN: B; PEPTIDE 5; CHAIN: C;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A, ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN, BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY CROSSREACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1

Table 5

SEQ ID No:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
964	1hxm	B	19	243	9e-57			242.19	GAMMA-DELTA T-CELL RECEPTOR CHAIN: A, C, E, G: GAMMA-DELTA T- CELL RECEPTOR; CHAIN: B, D, F, H;	IMMUNE SYSTEM T-CELL RECEPTOR DELTA CHAIN: T- CELL RECEPTOR GAMMA CHAIN; IG DOMAIN, T CELL RECEPTOR, TCR, GPCR
964	1hxm	B	1	84	8.4e-34			50.67	GAMMA-DELTA T-CELL RECEPTOR CHAIN: A, C, E, G: GAMMA-DELTA T- CELL RECEPTOR; CHAIN: B, D, F, H;	IMMUNE SYSTEM T-CELL RECEPTOR DELTA CHAIN: T- CELL RECEPTOR GAMMA CHAIN; IG DOMAIN, T CELL RECEPTOR, TCR, GPCR
964	1hzh	H	25	296	2.8e-83	0.11	-1202.08		IMMUNOGLOBULIN HEAVY CHAIN: CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN: CHAIN: L, M;	IMMUNE SYSTEM IGG, IMMUNOGLOBULIN, ANTIBODY, B12
964	1igt	B	145	296	1.4e-12	0.14	-1202.08		IGG2A INTACT ANTIBODY - MAR231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
964	1igt	B	24	283	8.4e-90	0.06	-1202.08		IGG2A INTACT ANTIBODY - MAR231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
964	1kx5	L	19	243	2.8e-70			109.47	KBS-CD2 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B, ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPHA V BETA DOMAIN; T- CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2
964	1hll	A	22	246	4.2e-69			114.77	LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN
964	1ngp	H	24	239	2.8e-82	0.09	-1202.08		NI69 (GGG)-LAMBDA-X CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
964	1wtl	A	1	101	4.2e-45			50.35	IMMUNOGLOBULIN WAT. A VARIABLE DOMAIN FROM IMMUNOGLOBULIN LIGHT-CHAIN 1WTL3 (GENE: JONES PROTEIN) 1WTL4	
964	25e8	H	24	239	4.2e-83	0.12	-1202.08		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTI-BODY, FAB, RING CLOSURE REACTION
964	2tb4	L	20	246	4.2e-67			109.74	IMMUNOGLOBULIN 2TB4 4	
964	2mg	I	20	246	9.8e-69			108.78	IMMUNOGLOBULIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCG3) 2MCG3 (TRIGONAL FORM) 2MCG4	
964	8fab	A	23	241	1.4e-69			118.67	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HLL) 8FAB 3	
968	1cdo	A	157	495	1.4e-78			91.38	ALCOHOL DEHYDROGENASE; ICDO 6 CHAIN: A, B; ICDO 7	OXIDOREDUCTASE (CH-OH/D)- NAD(P)+ OXIDOREDUCTASE ICDO 15
968	1cdo	A	164	492	1.4e-78	0.33	-1202.08		ALCOHOL DEHYDROGENASE; ICDO 6 CHAIN: A, B; ICDO 7	OXIDOREDUCTASE (CH-OH/D)- NAD(P)+ OXIDOREDUCTASE ICDO 15
968	1cdo	A	1	327	2.8e-69			82.11	ALCOHOL	OXIDOREDUCTASE (CH-OH/D)-

Table 5

SEQ ID NO.	PDB ID	CHAIN N/D	STAR T.AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DEHYDROGENASE; ICDO 6 CHAIN: A, B; ICDO 7	NAD(A) OXIDOREDUCTASE ICDO 15
968	1d1t	A	157	495	1.1e-80			92.65	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL, ROSSMANN OR DINUCLEOTIDE FOLD
968	1d1t	A	164	492	1.1e-80	0.32	-1202.08		ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL, ROSSMANN OR DINUCLEOTIDE FOLD
968	1d1t	A	3	327	5.6e-72			81.94	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL, ROSSMANN OR DINUCLEOTIDE FOLD
968	1d1t	A	110	495	8.4e-87			100.84	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL, ROSSMANN OR DINUCLEOTIDE FOLD
									HUMAN BETAI ALCOHOL DEHYDROGENASE; ICDO 7 CHAIN: A, B; ICDO 8	OXIDOREDUCTASE BETAI ADH; ICDO 9 NAD+ DEPENDENT ALCOHOL, DEHYDROGENASE ICDO 26
968	1d1t	A	164	492	8.4e-87	0.41	-1202.08		HUMAN BETAI ALCOHOL DEHYDROGENASE; ICDO 7 CHAIN: A, B; ICDO 8	OXIDOREDUCTASE BETAI ADH; ICDO 9 NAD+ DEPENDENT ALCOHOL, DEHYDROGENASE ICDO 26
968	1d1t	A	1	327	1.4e-78			87.63	HUMAN BETAI ALCOHOL DEHYDROGENASE; ICDO 7 CHAIN: A, B; ICDO 8	OXIDOREDUCTASE BETAI ADH; ICDO 9 NAD+ DEPENDENT ALCOHOL, DEHYDROGENASE ICDO 26
968	1d1t	A	106	495	7e-74			100.96	ALCOHOL DEHYDROGENASE; CLASS II CHAIN: A, B; ICDO 8	ALCOHOL, DEHYDROGENASE ICDO 15
968	1d1t	A	164	492	7e-74	0.38	-1202.08		ALCOHOL DEHYDROGENASE; CLASS II CHAIN: A, B; ICDO 8	ALCOHOL, DEHYDROGENASE ICDO 15

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOTOL D score	Compound	PDB annotation
									DEHYDROGENASE, CLASS II; CHAIN: A, B;	ALCOHOL DEHYDROGENASE
968	1c3i	A	3	327	56-67			82.29	ALCOHOL DEHYDROGENASE, CLASS II; CHAIN: A, B;	ALCOHOL DEHYDROGENASE
968	1c3j	A	163	491	146-60			82.26	NAD(PH)-DEPENDENT KETOSE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE
968	1c3j	A	1	323	286-58			78.55	NAD(PH)-DEPENDENT KETOSE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE
968	1het	A	110	495	426-83			94.36	ALCOHOL DEHYDROGENASE E; CHAIN: CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE I; OXIDOREDUCTASE(NAD(A)-CHOH(D))
968	1het	A	164	492	426-83	0.46	-1202.08		ALCOHOL DEHYDROGENASE E; CHAIN: CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE I; OXIDOREDUCTASE(NAD(A)-CHOH(D))
968	1het	A	3	327	286-75			79.40	ALCOHOL DEHYDROGENASE E; CHAIN: CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE I; OXIDOREDUCTASE(NAD(A)-CHOH(D))
968	1iso	A	110	495	76-87			101.16	CLASS I ALCOHOL DEHYDROGENASE I, ALPHA SUBUNIT; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE I, ALPHA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE
968	1iso	A	164	492	76-87	0.46	-1202.08		CLASS I ALCOHOL DEHYDROGENASE I, ALPHA SUBUNIT; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE I, ALPHA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE
968	1iso	A	1	327	146-78			89.46	CLASS I ALCOHOL DEHYDROGENASE I, ALPHA SUBUNIT; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE I, ALPHA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Peptide	Verify score	PMF score	SPOTOL D score	Compound	PDB annotation
968	1h0	A	110	495	4.2e-86			105.32	CHAIN: A, B; CLASS I ALCOHOL DEHYDROGENASE 3, GAMMA SUBUNIT; CHAIN: A, B;	ALCOHOL DEHYDROGENASE OXIDOREDUCTASE ALCOHOL DEHYDROGENASE (CLASS I), GAMMA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE, ZINC
968	1h0	A	164	492	4.2e-86	0.33	-1202.08		CLASS I ALCOHOL DEHYDROGENASE 3, GAMMA SUBUNIT; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE (CLASS I), GAMMA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE, ZINC
968	1h0	A	3	327	4.2e-78			90.30	CLASS I ALCOHOL DEHYDROGENASE 3, GAMMA SUBUNIT; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE (CLASS I), GAMMA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE, ZINC
968	1kav	A	1	325	9.8e-48			66.86	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE, ZINC, NADP
968	1qcr	A	165	495	2.8e-77			132.05	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH NADPH 100R 3	
968	1qcr	A	168	493	2.8e-77	0.62	-1202.08		OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH NADPH 100R 3	
968	1qcr	A	2	327	5.6e-78			128.24	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH	

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQIDOL D score	Compound	PDB annotation
968	1icf		11	162	0.008			52.38	NADPH 100R 3 TROPONIN G; CHAIN: N0LL.	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
968	1ieh	A	112	495	1.4e-90			100.75	HUMAN CHICK ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD- DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE
968	1ieh	A	164	492	1.4e-90	0.37	-1202.08		HUMAN CHICK ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD- DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE
968	1ieh	A	3	327	4.2e-78			85.11	HUMAN CHICK ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD- DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQPOL ID score	Compound	PDB annotation
968	1y1c	A	165	494	2.8e-58			68.99	NAD <sup>+</sup> -DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D.	DEHYDROGENASE OXIDOREDUCTASE OXIDOREDUCTASE
968	1y1c	A	1	326	1.4e-49			67.17	NAD <sup>+</sup> -DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D.	OXIDOREDUCTASE OXIDOREDUCTASE
968	7adh		1	327	5.6e-60			62.04	OXIDOREDUCTASE (NAD(P) <sup>+</sup> -CH(OH)(D)) ISONICOTINIMIDYLATE D LIVER ALCOHOL DEHYDROGENASE 7ADH 4 (B,C,1,1,1) 7ADHD 1 7ADHD 2	
970	1b1d		14	349	4.2e-59	0.14	-1202.08		BENZOTYLFORMATE DECARBOXYLASE; CHAIN: N1LL.	LYASE LYASE CARBON-CARBON DECARBOXYLASE, MANDULATE CATABOLISM, 2
970	1dw	A	1	316	8.4e-70			118.95	BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: A; BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: B.	OXIDOREDUCTASE THDP-BINDING FOLD, BRANCHED-CHAIN ALPHA-KETO ACID 2 DEHYDROGENASE
970	1dw	A	73	453	5.6e-70			161.96	BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: A; BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: B.	OXIDOREDUCTASE THDP-BINDING FOLD, BRANCHED-CHAIN ALPHA-KETO ACID 2 DEHYDROGENASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
970	Idlw	A	77	449	5.6e-70	0.44	-1202.08		BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: A; BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: B;	OXIDOREDUCTASE (THDP-BINDING FOLD, BRANCHED-CHAIN ALPHA-KETO ACID 2 DEHYDROGENASE
970	Ipxx	A	15	392	7e-40	0.22	-1202.08		OXIDOREDUCTASE(OX YGEN AS ACCEPTOR) PYRUVATE OXIDASE (E.C.1.2.3) MUTANT WITH PRO 178 IPOX 3 REPLACED BY SER, SER 188 REPLACED BY ASN, AND ALA 458 IPOX 4 REPLACED BY VAL (P178S,S188N,A458V) IPOX 5	
970	Ipxd	A	15	365	1.3e-46	0.06	-1202.08		LYASE (CARBON-CARBON) PYRUVATE DECARBOXYLASE (PDC) (E.C.4.1.1) IPVD 3	
970	Iqg0	A	121	446	2.8e-59	0.61	-1202.08		2-OXISOVALERATE DEHYDROGENASE ALPHA-SUBUNIT; CHAIN: A; 2-OXISOVALERATE DEHYDROGENASE BETA-SUBUNIT; CHAIN: B;	OXIDOREDUCTASE HETEROTETRAMER, THDP COFACTOR, OXIDOREDUCTASE
970	Iqg0	A	1	317	2.8e-59			91.32	2-OXISOVALERATE DEHYDROGENASE ALPHA-SUBUNIT; CHAIN: A; 2-OXISOVALERATE	OXIDOREDUCTASE HETEROTETRAMER, THDP COFACTOR, OXIDOREDUCTASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL ID score	Compound	PDB annotation
970	1q60	A	40	446	9e-76			140.12	DEHYDROGENASE BETA-SUBUNIT; CHAIN: B;	OXIDOREDUCTASE HETEROTETRAMER, THDP COFACTOR, OXIDOREDUCTASE
									2-OXOISOVALERATE DEHYDROGENASE ALPHA-SUBUNIT; CHAIN: A; 2- OXOISOVALERATE DEHYDROGENASE BETA-SUBUNIT; CHAIN: B;	
970	1q60	A	68	445	9e-76	0.55	-1202.08		2-OXOISOVALERATE DEHYDROGENASE ALPHA-SUBUNIT; CHAIN: A; 2- OXOISOVALERATE DEHYDROGENASE BETA-SUBUNIT; CHAIN: B;	OXIDOREDUCTASE HETEROTETRAMER, THDP COFACTOR, OXIDOREDUCTASE
									TRANSFERASE(KETONE RESIDUES) TRANSFEROLASE (E.C.2.1.1) TTRK 3	
970	1tkk	A	127	446	3e-57	0.16	-1202.08		IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
971	1a4f	A	24	139	1e-08	0.14	-1202.08		HEA-A-0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
971	1lk42	E	32	180	1.4e-67	0.07	-1202.08			

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Est Blast score	Verify score	PMF score	SEQ/ID score	Compound	PDB annotation
971	1be2	E	32	180	14e-67			86.31	CHAIN: E; HLA-A 0201; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
971	1bec		32	180	5.6e-66			81.96	14.3 D T CELL ANTIGEN RECEPTOR; IBEC 5 CHAIN: NULL; IBEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
971	1dk9	B	1	96	8.4e-38			57.60	T-CELL RECEPTOR D10 (ALPHA CHAIN); CHAIN: A; E; T-CELL RECEPTOR D10 (BETA CHAIN); CHAIN: B; E; MHC I-AK A CHAIN (ALPHA CHAIN); CHAIN: C; G; MHC I-AK B CHAIN (BETA CHAIN); CHAIN: D; H; CONALBUMIN PEPTIDE; CHAIN: P; Q;	IMMUNE SYSTEM MHC I-AK, MHC I-AK; T-CELL RECEPTOR, MHC CLASS II, D10, I-AK
971	1dk4	E	32	180	5.6e-61			81.57	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ HA1 PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-	IMMUNE SYSTEM HLA-DR1, DRA; HLA-DR1, DRB1 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Est Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
971	1ar1d	B	30	180	7e-64	0.19	-1202.08		CELL RECEPTOR BETA CHAIN; CHAIN: E;	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
971	1ar1f	B	30	180	7e-64			124.34	N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D, H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
971	1ar1g	B	30	180	7e-64				N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D, H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
971	1ar1h	B	30	180	1.3e-64	0.11	-1202.08		ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR: T-CELL RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
971	1ar1i	B	30	180	1.3e-64			73.51	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR: T-CELL RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
972	1ar1m	A	21	239	0.003			62.32	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
975	1ar1j	A	163	485	1.4e-18	0.07	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
975	1ar1k	A	182	532	9.8e-23			85.09	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
975	1ar1l	A	212	527	9.8e-23	0.18	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
975	1ar1m	A	410	580	2.8e-19	0.02	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1;	TRANSCRIPTION INHIBITOR BETA-PROPELLER

Table 5

SRC ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PAM score	SRC/ROL D score	Compound	PDB annotation
975	1g0t	B	227	567	14c-20			85.50	CHAIN: A, B, G; GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL, TRANSDUCTION
975	1g0t	B	305	579	14c-20	0.06	-1202.08		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL, TRANSDUCTION
977	1evu	A	108	710	9.8c-9l			142.67	PROSTAGLANDIN H2 SYNTHASE-2; CHAIN: A, B, 9-MER; CHAIN: F;	OXIDOREDUCTASE COX-2, CYCLOOXYGENASE, PROSTAGLANDIN, ARACHIDONATE, 2 ENDOPEXIDE
977	1evu	A	155	631	9.8c-9l	0.02	-1202.08		PROSTAGLANDIN H2 SYNTHASE-2; CHAIN: A, B, 9-MER; CHAIN: F;	OXIDOREDUCTASE COX-2, CYCLOOXYGENASE, PROSTAGLANDIN, ARACHIDONATE, 2 ENDOPEXIDE
977	1evu	A	6	584	0			142.21	PROSTAGLANDIN H2 SYNTHASE-2; CHAIN: A, B, 9-MER; CHAIN: F;	OXIDOREDUCTASE COX-2, CYCLOOXYGENASE, PROSTAGLANDIN, ARACHIDONATE, 2 ENDOPEXIDE
977	1dxv	A	132	235	1.5c-42			141.84	MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE;	OXIDOREDUCTASE HEME- PROTEIN, PEROXIDASE, OXIDOREDUCTASE



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
977	1d2v	A	6	109	2.8e-42			141.89	MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	PEROXIDASE-2 BROMIDE COMPLEX
								561.59	MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	OXIDOREDUCTASE HEME-PROTEIN, PEROXIDASE, PEROXIDASE-2 BROMIDE COMPLEX
977	1d2v	C	244	733	0				MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	OXIDOREDUCTASE HEME-PROTEIN, PEROXIDASE, PEROXIDASE-2 BROMIDE COMPLEX
977	1d2v	C	246	732	0	0.63	-1202.08		MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	OXIDOREDUCTASE HEME-PROTEIN, PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE-2 BROMIDE COMPLEX
977	1d2g	A	108	710	1.4e-93			148.59	PROSTAGLANDIN H2 SYNTHASE-1; CHAIN: A, B;	OXIDOREDUCTASE COX-1; RGF DOMAIN, NSAID BINDING, IBUPROFEN, MEMBRANE-BINDING 2 DOMAIN, CYCLOOXYGENASE, PEROXIDASE, OXIDOREDUCTASE, 3 DIOXYGENASE, PEROXIDASE
977	1d2g	A	1	584	2.8e-99			149.69	PROSTAGLANDIN H2 SYNTHASE-1; CHAIN: A, B;	OXIDOREDUCTASE COX-1; RGF DOMAIN, NSAID BINDING, IBUPROFEN, MEMBRANE-BINDING 2 DOMAIN, CYCLOOXYGENASE, PEROXIDASE, OXIDOREDUCTASE, 3 DIOXYGENASE, PEROXIDASE
981	1a2y	A	34	146	4.2e-40			59.18	MONOCLONAL ANTIBODY D1.3; CHAIN:	(IMMUNOGLOBULIN/HYDROLAS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
981	1a6v	H	34	150	1.1e-17			56.08	A, B: LYSOZYME; CHAIN: C;	B) COMPLEX (IMMUNOGLOBULIN/INTEGRALAS REGION, SIGNAL, HYDROLASE, GLYCOSIDASE, BACTERIOLYTIC 3 ENZYME, EGG WHITE
981	1a7q	L	1	101	1.4e-31			50.53	BI-8; CHAIN: L, H, M, L, N, J; MONOCLONAL ANTIBODY D1.3; CHAIN: L, H;	IMMUNOGLOBULIN, HAPTEN
981	1a7q	L	34	146	1.4e-38			59.67	MONOCLONAL ANTIBODY D1.3; CHAIN: L, H;	IMMUNOGLOBULIN, VARIANT
981	1a60	A	34	215	9.8e-60			55.26	ANTIBODY D1.3; CHAIN: L, H;	IMMUNOGLOBULIN, VARIANT
981	1a6q	L	36	203	2.8e-68	0.25	-1202.08		FAB FRAGMENT ANTIBODY A5B7; CHAIN: A, B, C, D; IGG4 REA; CHAIN: A, RE-ANTIGEN/LAMBD4; CHAIN: H, L;	IMMUNOGLOBULIN, FAB FRAGMENT
981	1a67	E	36	215	1.5e-12			61.51	HLA-A*0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN, RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
981	1a6k	L	36	203	1.4e-62	0.10	-1202.08		FAB B7-15A2; CHAIN: L, H;	IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH

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Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR TAA	END AA	Int Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
981	1at1	D	34	146	146-35			56.21	CYTOCHROME C OXIDASE; CHAIN: A, B; ANTIBODY FV FRAGMENT; CHAIN: C, D;	AFINITY CRYSTAL 2 PACKING MOTIF PROGRAMMING PROFENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN
981	1b0w	A	34	153	2,86-43			55.87	BENCE-JONES KAPPA I PROTEIN BREE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN; ANTILLOID; IMMUNE SYSTEM
981	1b2w	L	34	198	2,86-62	0.16	-1202.08		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X- RAY STRUCTURE, THREE- DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
981	1b6d	A	34	198	4,26-62	0.10	-1202.08		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN KAPPA LIGHT-CHAIN DIMER HEADER
981	1b6d	D	35	214	76-20			55.30	HLA-A 0201; CHAIN: A; B*7A-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA;	COMPLEX (IMMUNOGLOBULIN PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (IMMUNOGLOBULIN PEPTIDE/RECEPTOR)

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Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: D, T CELL RECEPTOR BETA; CHAIN: E;	
981	1bj1	J	34	198	9,8e-64	0.18	-1202.08		FAB FRAGMENT; CHAIN: L, H, L, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12, VEGF, COMPLEX (ANTIBODY/ANTIGEN) ANGIOGENIC FACTOR
981	1bjk	A	34	146	1,4e-44			55.47	HULYSLI; CHAIN: A, B, D, E, LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, PV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
981	1bwv	A	32	147	5,6e-45			57.52	IG KAPPA CHAIN V-L REGION RE; CHAIN: A <sub>6</sub> B <sub>1</sub>	IMMUNE SYSTEM REV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM ANTIBODY, THERAPEUTIC, ANTIBODY, CD52
981	1ce1	L	34	215	8,4e-61			55.66	CAMPATH-1H LIGHT CHAIN; CHAIN: L; CAMPATH-1H HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	
981	1dee	A	34	198	1,4e-63	0.23	-1202.08		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-1BP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VIRB 3 SPECIFICITY
981	1dfb	L	34	215	5,6e-60			55.96	IMMUNOGLOBULIN 3D6 FAB 1DDB 3	

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T.AA	END AA	Pst Blast	Verity score	PMF score	SIQPOL D score	Compound	PDB annotation
981	1dm0	A	35	198	2.8e-62	0.25	-1202.08		IGM-KAPPA COLD AGGLUTININ (LIGHT CHAIN); CHAIN: A, C; IGM-KAPPA COLD AGGLUTININ (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM FAB, IGM, ANTIBODY, COLD AGGLUTININ, HUMAN
981	1fgv	L	1	102	7e-41			50.49	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY H52 (HUH52-AA FV) IFGV 4	
981	1fgv	L	34	146	1.3e-46			57.40	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY H52 (HUH52-AA FV) IFGV 4	
981	1bkm	B	34	215	4.2e-25			57.17	GAMMA-DELTA T-CELL RECEPTOR; CHAIN: A, C, E, G, GAMMA-DELTA T-CELL RECEPTOR; CHAIN: B, D, F, H;	IMMUNE SYSTEM T-CELL RECEPTOR DELTA CHAIN, T-CELL RECEPTOR GAMMA CHAIN, IG DOMAIN, T CELL RECEPTOR, TCR, GDTOR
981	1lgn	L	34	155	4.2e-46			59.49	IMMUNOGLOBULIN M (IG-M) FV FRAGMENT IIGM 3	
981	1jth	L	34	206	1.4e-45			56.13	ANTIBODY A6; CHAIN: L, H; INTERFERON-GAMMA RECEPTOR ALPHA CHAIN; CHAIN: I;	COMPLEX (ANTIBODY/ANTIGEN) CYTOKINE RECEPTOR, COMPLEX (ANTIBODY/ANTIGEN), 2 TRANSMEMBRANE, CYCLOPROTEIN
981	1lht	A	36	203	8.4e-65	0.07	-1202.08		LAMBDA III BENCE JONES PROTEIN (L); CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
981	1ngp	H	34	215	4.2e-23			56.17	NIG9 (IGG1= $\lambda$ MBDA=); CHAIN: L, H	IMMUNOGLOBULIN
981	1plg	H	34	215	2.8e-18			56.05	IGG2A-KAPPA=, 1PLG 4 CHAIN: L, H, 1PLG 5	IMMUNOGLOBULIN
981	1ter	A	35	215	7e-20			57.82	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR FOR T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
981	2fgw	L	34	198	9.8e-64	0.07	-1202.08		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY H52 (RUH52-OZ FAB) 2FGW 4	
981	2fgw	L	34	215	9.8e-64			56.05	IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY H52 (RUH52-OZ FAB) 2FGW 4	
								54.90	IMMUNOGLOBULIN; CHAIN: A, B, C, D;	IMMUNOGLOBULIN
981	2gpp	B	34	215	9.8e-19				IMMUNOGLOBULIN; CHAIN: A, B, C, D;	IMMUNOGLOBULIN
981	8fab	A	38	203	4.2e-66	0.13	-1202.08		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN	
									IMMUNOGLOBULIN IGG1 ( $\lambda$ MBDA, HIL) 8FAB 3	
981	8fab	A	38	215	4.2e-66			55.65	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN	
									IMMUNOGLOBULIN IGG1 ( $\lambda$ MBDA, HIL) 8FAB 3	
982	12e8	L	24	224	1.4e-74			96.49	2E8 (IGG1-KAPPA=)	IMMUNOGLOBULIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEOTOL D score	Compound	PDB annotation
982	1a4j	A	23	238	9.8e-72			98.04	ANTIBODY; CHAIN: L, H, M, F;	IMMUNOGLOBULIN
									IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
982	1a07	D	1	97	1.3e-35			70.96	HLA-A*0201; CHAIN: A, BETA-2	COMPLEX (MHC/ANTAL PEPTIDE/RECEPTOR) HLA-A2
									HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIBAL PEPTIDE, 2 COMPLEX (MHC/ANTAL PEPTIDE/RECEPTOR	
									CHAIN: D, T CELL RECEPTOR, BETA, CHAIN: B;	
982	1b2w	L	22	224	1.4e-81			98.81	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM
									IMMUNOGLOBULIN, ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2X-RAV STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM	IMMUNOGLOBULIN, ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2X-RAV STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
982	1b6d	A	22	222	1.4e-81	0.00	-1202.08		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN
									IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER, HEADER	IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER, HEADER
982	1b6d	A	22	233	1.4e-81			96.63	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER, HEADER
									T CELL RECEPTOR, T CELL RECEPTOR, MHC CLASS I, HUMAN IMMUNODEFICIENCY VIRUS, 2 MOLECULAR RECOGNITION	T CELL RECEPTOR, T CELL RECEPTOR, MHC CLASS I, HUMAN IMMUNODEFICIENCY VIRUS, 2 MOLECULAR RECOGNITION
982	1b88	A	1	97	1.1e-40			83.05	T CELL RECEPTOR V-ALPHA DOMAIN; CHAIN: A, B;	

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Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
982	1bc2	D	22	218	3c-74			230.06	HLA-A*0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E	COMPLEX (MICROVIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MICROVIRAL PEPTIDE/RECEPTOR)
982	1bj1	J	22	223	11c-83	0.15	-1202.08		FAB FRAGMENT; CHAIN: L; H; J; K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V; W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; YEGH: COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
982	1ce1	L	22	232	14c-79			97.53	CAMPATH-1H/IGHT CHAIN: CHAIN: L; CAMPATH-1H/HEAVY CHAIN: CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
982	1ce	A	24	224	14c-74			96.33	IG HEAVY CHAIN V REGIONS: CHAIN: A; IG HEAVY CHAIN V REGIONS: CHAIN: B; IG HEAVY CHAIN V REGIONS: CHAIN: C; IG HEAVY CHAIN V REGIONS: CHAIN: D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB COMPLEX, IDIOTOPE, ANTI- IDIOTOPE
982	1dc	A	1	97	28c-42			79.58	T-CELL RECEPTOR D10 (ALPHA CHAIN); CHAIN: A; E; T-CELL RECEPTOR D10 (BETA CHAIN); CHAIN: B; F; MHC I-A* A CHAIN (ALPHA CHAIN);	IMMUNE SYSTEM MHC I-A*; MHC I-A* T-CELL RECEPTOR, MHC CLASS II D10, I-A* K



Table 5

SEQ ID NO.	PDB ID	CHAIN N ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEOPOL D score	Compound	PDB annotation
982	1dce	A	22	226	1.4e-84			96.48	CHAIN: C, G, MHC I-AK B CHAIN (BETA CHAIN), CHAIN: D, H, CONALBUMIN PEPTIDE, CHAIN: P, Q.	IMMUNE SYSTEM FAB-BIP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
982	1dlp	A	12	304	5.6e-92			130.53	DIHYDRODIPICOLINATE SYNTHASE, CHAIN: A, B.	DIHYDRODIPICOLINATE SYNTHASE DHPS: SYNTHASE, DIHYDRODIPICOLINATE
982	1da0	A	22	223	2.8e-79	0.02	-1202.08		IGM-KAPPA COLD AGGLUTININ (LIGHT CHAIN), CHAIN: A, C, IGM-KAPPA COLD AGGLUTININ (HEAVY CHAIN), CHAIN: B, D.	IMMUNE SYSTEM FAB, IGM, ANTIBODY, COLD AGGLUTININ, HUMAN
982	1dck	L	22	224	1.4e-74			97.96	TAB2, CHAIN: L, M, TAB2, CHAIN: H, I, CYCLIC PEPTIDE, CHAIN: P, Q.	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN-PEPTIDE RECOGNITION
982	1dgl	L	24	221	1.4e-73			100.34	CYTOKINE RECEPTOR COMANON BETA CHAIN PRECURSOR, CHAIN: A, ANTIBODY (LIGHT CHAIN), CHAIN: L, ANTIBODY (HEAVY CHAIN), CHAIN: H.	IMMUNE SYSTEM CYTOKINE RECEPTOR COMPLEXED TO AN ANTIBODY
982	1ent	L	22	224	1.3e-75			98.73	IGG ANTIBODY (LIGHT CHAIN), CHAIN: L, IGG ANTIBODY (HEAVY CHAIN), CHAIN: H.	IMMUNE SYSTEM ANTI-FULLEIRINE ANTIBODY, NANOTUBES

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
982	1fg	L	21	224	7e-75			97.87	IMMUNOGLOBULIN (KAPPA LIGHT CHAIN) FAB FRAGMENT 1FG3	
982	1fms	L	22	224	8.4e-78			96.30	IMMUNOGLOBULIN NM4-1GG1; CHAIN: L; IMMUNOGLOBULIN NM4-1GG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A-ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
982	1fvd	A	22	223	7e-81	0.31	-1202.08		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4DS, VERSION 4 1FVD 3	
982	1fvt	D	22	218	2.8e-57			204.11	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ H1 PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR BETA CHAIN; CHAIN: E;	IMMUNE SYSTEM HLA-DR1, DR4, HLA-DR1, DRB1 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD
982	1ghn	L	21	227	1.4e-77			97.48	ENVULOPE GLYCOPROTEIN GP120; CHAIN: G; T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: C; ANTIBODY 17B, LIGHT CHAIN;	VIRUS/VIRAL PROTEIN COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120 FROM LABORATORY-ADAPTED ISOLATE, HXB2, 3 SURFACE T-CELL GLYCOPROTEIN CD4,

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Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Bias	Verify score	PMF score	SEOROL D score	Compound	PDB annotation
982	1l7z	A	24	224	2.8c-76			98.87	CHAIN: L; ANTIBODY 17B; HEAVY CHAIN; CHAIN: H; CHIMERA OF IG KAPPA CONSTANT REGION CHAIN: A; C; CHIMERA OF IG GAMMA-1 CHAIN: HUMAN CONSTANT CHAIN: B, D	ANTIGEN-BINDING FRAGMENT 4 OF HUMAN IMMUNOGLOBULIN 17B
982	1l85	A	1	97	5.6c-43			87.06	KBS-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A; B; ANTIBODY DESIRE-1; CHAIN: L; H;	COMPLEX (IMMUNOGLOBULIN RECEPTOR) TCR VAP/HA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLOTOTYPIC, 2
982	1qzn	D	23	221	1.2c-77			239.88	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; T-CELL RECEPTOR, ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR, BETA CHAIN; CHAIN: E; IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 (HCHS2-OZ FAB) 2PGW 4	IMMUNE SYSTEM MHC CLASS I HLA-A; MHC CLASS I ANTIGEN; A6-TCR; TCR BETA CHAIN; HUMAN TCR/PEPTIDEMHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR
982	2l6w	L	22	223	7c-83	0.04	-1202.08		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 (HCHS2-OZ FAB) 2PGW 4	
982	1l66	B	221	337	9.8c-10	0.35	-1202.08		ARYLAALKYLAMINE N-	TRANSFRASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEDOU, D score	Compound	PDB annotation
									ACETYLTRANSFERASE; CHAIN: A, B;	ACETYLTRANSFERASE
983	1q1w	A	221	337	1.1e-08	0.14	-1202.08		SEROTONIN N-ACETYLTRANSFERASE; CHAIN: A;	TRANSFERASE
983	1b1	E	221	337	1.1e-08	0.20	-1202.08		14-3-3 ZETA ISOFORM; CHAIN: A, B, C, D; SEROTONIN N-ACETYLTRANSFERASE; CHAIN: E, F, G, H;	SIGNALING PROTEIN/TRANSFERASE PROTEIN KINASE C INHIBITOR, PROTEIN-1; ARALKYLAMINE N-ACETYLTRANSFERASE, AA-NAT, N-ACETYLTRANSFERASE, 14-3-3, SIGNAL, TRANSDUCTION, PROTEIN-2 PROTEIN COMPLEX, PHOSPHORYLATION
983	1qam	A	218	334	9.8e-14	0.03	-1202.08		HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX
983	1ext	A	38	209	1.4e-10			53.75	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
983	1ext	A	52	202	1.4e-10	0.25	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
983	1g44	A	44	258	3e-07			57.93	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
983	1g44	B	31	250	0.0006			60.13	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
983	1bqj		9	84	1.1e-29			70.79	HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HD-1;
983	1lgf	A	40	171	1.5e-09	0.21	-1202.08		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Bias	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
983	1k0		44	221	7e-13			55.87	LAMININ; CHAIN: NULL.	GLYCOPROTEIN GLYCOPROTEIN
983	1inf	A	52	179	8.4e-09	0.15	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	SIGNALING PROTEIN TYPE I RECEPTOR; STNRP1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19
983	9wga	A	45	224	7e-14			51.43	LECTIN (AGGELUTININ) WHEAT GERM AGGELUTININ (ISOLECTIN 2); 9WGA 3	
987	1afy	A	127	368	1.2e-40	0.46	-1202.08		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B; E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
987	1afy	A	246	375	1.2e-19	0.23	-1202.08		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B; E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
987	1afy	A	54	355	7.5e-45	0.39	-1202.08		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B; E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE); COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
987	1afn	A	108	283	1.3e-28	0.31	-1202.08		U2 RNA HAIRPIN IV; CHAIN: O, R; U2 A;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T.A.A	EVD AA	Pst Blast	Verify score	PMF score	SEQ/POI. D score	Compound	PDB annotation
987	1a9n	A	179	330	1.4e-30	0.79	-1202.08		CHAIN: A, C; U2 B <sup>+</sup> ; CHAIN: B, D;	(NUCLEAR PROTEIN/RNA, RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	A	203	355	1e-32	0.59	-1202.08		UD RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>1</sub> ; CHAIN: A, C; U2 B <sup>+</sup> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	A	276	368	1.4e-15	0.31	-1202.08		UD RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>1</sub> ; CHAIN: A, C; U2 B <sup>+</sup> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	A	54	213	1.5e-21	0.15	-1202.08		UD RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>1</sub> ; CHAIN: A, C; U2 B <sup>+</sup> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	A	83	233	1.2e-29	0.46	-1202.08		UD RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>1</sub> ; CHAIN: A, C; U2 B <sup>+</sup> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	108	283	1.5e-28	0.13	-1202.08		UD RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>1</sub> ; CHAIN: A, C; U2 B <sup>+</sup> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	179	327	9e-31	0.73	-1202.08		UD RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>1</sub> ; CHAIN: A, C; U2 B <sup>+</sup> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	203	355	6e-32	0.50	-1202.08		UD RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>1</sub> ; CHAIN: A, C; U2 B <sup>+</sup> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SNRNP, RIBONUCLEOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Pst Blast	Verfity score	PMF score	SEQ/POU D score	Compound	PDB annotation
987	1d0h	C	273	369	1.5e-15	0.36	-1202.08		UD RNA HAIRPIN IV; CHAIN: A, C; UD A; CHAIN: A, C; UD B; CHAIN: B, D.	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA, RNA, SNRNP RIBONUCLEOPROTEIN
987	1d0h	C	54	233	9e-22	0.11	-1202.08		UD RNA HAIRPIN IV; CHAIN: Q, R; UD A; CHAIN: A, C; UD B; CHAIN: B, D.	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA, RNA, SNRNP RIBONUCLEOPROTEIN
987	1a9n	C	83	231	1.5e-29	0.50	-1202.08		UD RNA HAIRPIN IV; CHAIN: Q, R; UD A; CHAIN: A, C; UD B; CHAIN: B, D.	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA, RNA, SNRNP RIBONUCLEOPROTEIN
987	1d0b	A	110	329	4.5e-37		71.98		INTERNALIN B; CHAIN: A;	CELL ADHESION (LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	170	368	7.5e-34	1.01	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION (LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	244	423	1.3e-20	0.78	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION (LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	279	433	5.0e-15	0.33	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION (LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	33	204	7e-22	0.30	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION (LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	48	232	3e-27	0.29	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION (LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	61	279	4.5e-37	0.63	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION (LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	63	252	2.8e-26	0.41	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION (LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION

Table 5

SRC ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Pi Blast	Verify score	PMF score	SRCOROL D score	Compound	PDB annotation
									A;	REPEAT, CALCIUM BINDING, CELL ADHESION
987	1de	A	272	381	2.8e-13	0.56	-1202.08		RAB GERANYLGERANYLT NSFERASE ALPHA SUBUNIT; CHAIN: A, C RAB GERANYLGERANYLT NSFERASE BETA SUBUNIT; CHAIN: B, D	TRANSFERRASE CRYSTAL STRUCTURE; RAB GERANYLGERANYLT NSFERASE ALPHA E, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
987	1601	B	228	369	9e-17	0.07	-1202.08		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP RBD OR RRM) AND LEUCINE-RICH REPEAT 2 (LRR)
987	16q	A	183	380	9e-20	0.25	-1202.08		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN ACDC2- ASSOCIATED PROTEIN P45; CYCLIN ACDC2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
987	16q	A	71	400	7.5e-25			69.13	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN ACDC2- ASSOCIATED PROTEIN P45; CYCLIN ACDC2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
987	16s2	A	187	385	3e-15	0.13	-1202.08		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN ACDC2- ASSOCIATED P45; CYCLIN ACDC2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE- RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
987	16s2	A	53	321	1.5e-18	0.03	-1202.08		SKP2; CHAIN: A, C; SKP1;	LIGASE CYCLIN ACDC2-



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pd Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
987	1yrg	A	126	371	7.5e-28	0.12	-1202.08		CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDC2-ASSOCIATED P19; SKP1, SKP2, E-BOX, LRRS, LEUCINE- RICH REPEATS, SCF 2 UBIQUITIN, ES, UBIQUITIN PROTEIN LIGASE
									CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPL; GTPASE-ACTIVATING PROTEIN; GAP; RNAIP; RANGAP LRR; LEUCINE-2 RICH REPEAT PROTEIN; TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
987	1yrg	A	57	390	9e-34			70.31	GTPASE-ACTIVATING PROTEIN RNAL_SCFPO, CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPL; GTPASE-ACTIVATING PROTEIN; GAP; RNAIP; RANGAP LRR; LEUCINE-2 RICH REPEAT PROTEIN; TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
										TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPL; GTPASE-ACTIVATING PROTEIN; GAP; RNAIP; RANGAP LRR; LEUCINE-2 RICH REPEAT PROTEIN; TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
987	1yrg	A	59	185	3e-14	0.21	-1202.08		GTPASE-ACTIVATING PROTEIN RNAL_SCFPO, CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPL; GTPASE-ACTIVATING PROTEIN; GAP; RNAIP; RANGAP LRR; LEUCINE-2 RICH REPEAT PROTEIN; TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
										TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPL; GTPASE-ACTIVATING PROTEIN; GAP; RNAIP; RANGAP LRR; LEUCINE-2 RICH REPEAT PROTEIN; TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
987	1yrg	A	75	282	3e-29	0.33	-1202.08		GTPASE-ACTIVATING PROTEIN RNAL_SCFPO, CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPL; GTPASE-ACTIVATING PROTEIN; GAP; RNAIP; RANGAP LRR; LEUCINE-2 RICH REPEAT PROTEIN; TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pd Blast	Verity score	PMF score	SEOFOL D score	Compound	PDB annotation
987	1yre	A	94	330	9c-34	0.48	-1202.08		GTPASE-ACTIVATING PROTEIN RNAL_SCHPO; CHAIN: A, B;	ACTIVATING PROTEIN, GAP, RNAP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL, TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
987									RANGAP: GTPASE-ACTIVATING PROTEIN FOR SPIL, GTPASE-ACTIVATING PROTEIN, GAP, RNAP, RANGAP LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL, TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY	
987	2mhl		80	368	1.3c-48	0.52	-1202.08		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
988	1ap2	A	103	359	1.4e-58	0.45	-1202.08		NITROGENASE IRON PROTEIN; CHAIN: A, B;	OXIDOREDUCTASE CP2; OXIDOREDUCTASE, NITROGENASE IRON PROTEIN HEADER CONNECT LINK
988	1ap2	A	104	359	1.4e-58			64.61	NITROGENASE IRON PROTEIN; CHAIN: A, B;	OXIDOREDUCTASE CP2; OXIDOREDUCTASE, NITROGENASE IRON PROTEIN HEADER CONNECT LINK
988	1tp6	A	100	359	9.8c-61			58.49	NITROGENASE IRON PROTEIN; CHAIN: A, B, C, D;	OXIDOREDUCTASE NITROGENASE COMPONENT II, NITROGENASE REDUCTASE, NITROGENASE, NITROGEN FIXATION, NUCLOTIDE, MGADP, PE 2 PROTEIN, AY2
988	1tp6	A	103	359	9.8c-61	0.56	-1202.08		NITROGENASE IRON	OXIDOREDUCTASE

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Est Blast	Verify score	PMF score	SEQ/PROL D score	Compound	PDB annotation
988	1hp5	A	104	359	3e-46	0.35	-1202.08		PROTEIN; CHAIN: A, B, C, D;	NITROGENASE COMPONENT II, NITROGENASE REDUCTASE, NITROGENASE, NITROGEN FIXATION, NUCLOTIDE, MGADP, FE 2 PROTEIN, AV2
988	1hs		19	296	1.1e-06			53.22	FTSY; CHAIN: NULL;	NITROGENASE COMPONENT II, NITROGENASE REDUCTASE, NITROGENASE, NITROGEN FIXATION, NUCLOTIDE, MGADP, FE 2 PROTEIN, AV2
988	1g20	E	103	359	1.4e-57	0.22	-1202.08		NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN; CHAIN: A, C; NITROGENASE MOLYBDENUM-IRON PROTEIN BETA CHAIN; CHAIN: B, D; NITROGENASE IRON PROTEIN; CHAIN: E, F, G, H;	OXIDOREDUCTASE NITROGENASE COMPONENT I, DINITROGENASE, NIFD, NITROGENASE COMPONENT I, DINITROGENASE, NIFK, NITROGENASE COMPONENT II, NITROGENASE REDUCTASE, NITROGEN-FIXATION, FE PROTEIN, MOFE PROTEIN, P- CLUSTER AND 2 PEMO COF ACTOR
988	1g20	E	104	359	1.4e-57			62.01	NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN; CHAIN: A, C; NITROGENASE MOLYBDENUM-IRON PROTEIN BETA CHAIN; CHAIN: B, D;	OXIDOREDUCTASE NITROGENASE COMPONENT I, DINITROGENASE, NIFD, NITROGENASE COMPONENT I, DINITROGENASE, NIFK, NITROGENASE COMPONENT II, NITROGENASE REDUCTASE, NITROGEN-FIXATION, FE



Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T.AA	END AA	PsI Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
988	1h2c	E	100	359	9.8e-61			64.02	NITROGENASE MOLYBDENUM-IRON PROTEIN; CHAIN: A, B, C, D; NITROGENASE; IRON PROTEIN; CHAIN: E, F, G, H;	COMPLEX OF NITROGENASE PROTEINS NITROGENASE COMPONENT 1, DNITROGENASE, NITROGENASE COMPONENT 1L, NITROGENASE REDUCTASE; NITROGENASE, NITROGEN FIXATION, SIGNAL TRANSDUCTION, 2 ELECTRON TRANSFER, ATP HYDROLYSIS, COMPLEX OF NITROGENASE 3 PROTEINS
988	1h2c	E	103	359	9.8e-61	0.41	-1202.08		NITROGENASE MOLYBDENUM-IRON PROTEIN; CHAIN: A, B, C, D; NITROGENASE; IRON PROTEIN; CHAIN: E, F, G, H;	COMPLEX OF NITROGENASE PROTEINS NITROGENASE COMPONENT 1, DNITROGENASE, NITROGENASE COMPONENT 1L, NITROGENASE REDUCTASE; NITROGENASE, NITROGEN FIXATION, SIGNAL TRANSDUCTION, 2 ELECTRON TRANSFER, ATP HYDROLYSIS, COMPLEX OF NITROGENASE 3 PROTEINS
989	1aut	L	605	684	1.4e-11	0.03	-1202.08		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION(INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION(INHIBITOR)
989	1ccv	A	628	682	1.3e-14	0.42	-1202.08		CHYMOTRYPSIN INHIBITOR; CHAIN: A;	HYDROLASE INHIBITOR, AMCI PROTEIN INHIBITOR, HEXONYMPH, APS MML1, LIBERA, CANONICAL 2 INHIBITOR
989	1dva	L	146	229	5.6e-11	0.04	-1202.08		DES-GI.A FACTOR, VIIA	HYDROLASE/HYDROLASE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PVAL score	SEOFOL D score	Compound	PDB annotation
989	1tak	L	182	259	4.2e-12	0.02	-1202.08		(HEAVY CHAIN)-CHAIN: H, I, DES-GLA FACTOR VITA (LIGHT CHAIN)-CHAIN: L, M, (DPN)-PHE-ARG-CHAIN: C, D, PEPTIDE E-76-CHAIN: X, Y.	INHIBITOR PROTEIN-PEPTIDE COMPLEX
989	1tak	L	182	259	4.2e-12	0.02	-1202.08		BLOOD COAGULATION FACTOR VILA: CHAIN: L; BLOOD COAGULATION FACTOR VILA: CHAIN: H; SOLUBLE TISSUE FACTOR: CHAIN: T; SLI5; CHAIN: I; PROTEASE/COFACTOR(LIGAND), BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR(LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, BGR, COMPLEX (SERINE 4) PROTEASE/COFACTOR(LIGAND), BLOOD CLOTTING	
989	1bx2	A	628	682	9e-18	0.33	-1202.08		BST1; CHAIN: A; BOMBINA SKIN TRYPSIN INHIBITOR BETA-SHEET DISULFIDE-RICH	HYDROLASE INHIBITOR BOMBINA SKIN TRYPSIN INHIBITOR BETA-SHEET DISULFIDE-RICH
989	1qub	A	89	364	6e-15	0.05	-1202.08		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHL, COMPLEMENT CONTROL, PROTEIN, 2-N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
992	1a3r	L	20	221	9.8e-83	0.69	-1202.08		IGG2A; CHAIN: L, H; HUMAN RHEINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	COMPLEX (IMMUNOGLOBULIN VIRAL PEPTIDE) ANTIBODY 855; IMMUNOGLOBULIN, ANTIBODY, RHEINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPIPTOPE, COMPLEX (IMMUNOGLOBULIN VIRAL

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
992	1a9k	L	21	221	66-86	0.91	-1202.08		FAB B7-15A2; CHAIN: L <sub>1</sub>	PEPTIDE IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN
992	1a9k	L	21	222	66-86			222.04	FAB B7-15A2; CHAIN: L <sub>1</sub>	IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN
992	1b1m	A	20	222	36-83			228.10	LOC - LAMBDA 1 TYPE LIGHT-CHAIN DIMER; IBIM 6 CHAIN: A, B; IBIM 7	IMMUNOGLOBULIN BENCE-JONES PROTEIN; IBIM 8 BENCE JONES ANTIBODY, MULTIPLE QUATERNARY STRUCTURES IBIM 13
992	1b1m	A	21	221	1,36-74	0.92	-1202.08		LOC - LAMBDA 1 TYPE LIGHT-CHAIN DIMER; IBIM 6 CHAIN: A, B; IBIM 7	IMMUNOGLOBULIN BENCE-JONES PROTEIN; IBIM 8 BENCE JONES ANTIBODY, MULTIPLE QUATERNARY STRUCTURES IBIM 13
992	1b1m	A	21	221	36-83	1.01	-1202.08		LOC - LAMBDA 1 TYPE LIGHT-CHAIN DIMER; IBIM 6 CHAIN: A, B; IBIM 7	IMMUNOGLOBULIN BENCE-JONES PROTEIN; IBIM 8 BENCE JONES ANTIBODY, MULTIPLE QUATERNARY STRUCTURES IBIM 13
992	1dbb	A	3	129	1,46-44	0.74	-1202.08		SCFV FRAGMENT 1P9; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	COMPLEX (ANTIBODY ANTIGEN) 1,4-BETA-N-ACETYLAMINAMIDASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pg Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
992	1h1	A	20	221	4.2e-83	0.76	-1202.08		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) IHL 3	
992	1h1	A	20	222	4.2e-83			155.83	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) IHL 3	
992	1ih	L	20	221	4.2e-83	0.78	-1202.08		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) COMPLEX WITH PEPTIDE OF IIFH 3 INFLUENZA HEMAGGLUTININ HA1 (STRAIN X47) (RESIDUES 101-107) IIFH 4	
992	1ih	L	20	222	4.2e-83			155.98	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) COMPLEX WITH PEPTIDE OF IIFH 3 INFLUENZA HEMAGGLUTININ HA1 (STRAIN X47) (RESIDUES 101-107) IIFH 4	
992	1hpb	A	12	130	1.4e-45	0.93	-1202.08		SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	IMMUNOGLOBULIN VARIABLE HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT MULTIVALENT ANTIBODY DIABODY, DOMAIN 2 SWAPPING, IMMUNOGLOBULIN
992	1gok	A	12	129	7e-46	1.09	-1202.08		MFE-23 RECOMBINANT ANTIBODY FRAGMENT; CHAIN: A;	IMMUNOGLOBULIN CHAIN FV, ANTI-CARCINOEMBRYONIC 2 ANTIGEN MONOCLONAL ANTIBODY
992	1abs	L	20	221	1.4e-84	0.73	-1202.08		MONOCLONAL	MONOCLONAL ANTIBODY



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
992	15b6	L	20	222	1.4e-84			158.44	ANTIBODY 3A2, CHAIN: H, L; MONOCLONAL ANTIBODY 3A2, CHAIN: H, L; IMMUNOGLOBULIN FAB	MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
992	2B4	L	20	221	7e-77	0.96	-1202.08		IMMUNOGLOBULIN FAB	
992	2B4	L	20	222	7e-77			238.13	IMMUNOGLOBULIN FAB	
992	2mcg	L	1	98	4.2e-51			88.32	IMMUNOGLOBULIN FAB	
									IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCG3) 2MCG 3 (TRIGONAL FORM)	
992	2mcg	L	20	222	1.3e-82			208.98	IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCG3) 2MCG 3 (TRIGONAL FORM)	
									IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCG3) 2MCG 3 (TRIGONAL FORM)	
992	2mcg	L	21	221	1.3e-82	0.86	-1202.08		IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCG3) 2MCG 3 (TRIGONAL FORM)	
									IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCG3) 2MCG 3 (TRIGONAL FORM)	
992	7fab	L	20	222	4.5e-78			203.84	IMMUNOGLOBULIN FAB-NEW LAMBDA LIGHT CHAIN) 7FAB 3	
992	7fab	L	21	221	4.5e-78	0.91	-1202.08		IMMUNOGLOBULIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T A A	END A A	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
									IMMUNOGLOBULIN F <sub>AB</sub> NEW (LAMBDA LIGHT CHAIN) YEAB 3	
994	12e8	L	28	215	4.2e-09			63.88	IMMUNOGLOBULIN 2ER (UGG [=KAPPA-])	IMMUNOGLOBULIN
	1a4f	A	28	232	5.6e-11			63.22	IMMUNOGLOBULIN, M <sub>1</sub> P <sub>1</sub>	IMMUNOGLOBULIN
994	1a4f	A	28	232	5.6e-11			63.22	IMMUNOGLOBULIN, DIELS ALDER	IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER 2 GRMULNE
994	1a40	A	28	234	5.6e-13			64.06	IMMUNOGLOBULIN, F <sub>AB</sub> FRAGMENT, ANTIBODY ASBT, CHAIN: A, B, C, D	IMMUNOGLOBULIN, F <sub>AB</sub> FRAGMENT
994	1b2w	L	28	234	2.8e-11			68.36	IMMUNOGLOBULIN, ANTIBODY (LIGHT CHAIN), CHAIN: L, ANTIBODY (HEAVY CHAIN), CHAIN: H	IMMUNE SYSTEM, IMMUNOGLOBULIN, IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, F <sub>AB</sub> , 2X-RAY STRUCTURE, TERE- DIMENSIONAL STRUCTURE, GAMMA- 3 INTERFERON
									IMMUNE SYSTEM	
994	1b4f	L	28	232	5.6e-13			68.55	ANTIBODY; CHAIN: L, H	ANTIBODY ENGINEERING, ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODIES, 2FAB, X-RAY STRUCTURES, GAMMA- INTERFERON
994	1b1h	A	2	306	1.4e-40	0.04	-1202.08		HEMOLIN; CHAIN: A, B	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HEMOPHILIC ADHESION
994	1cdy		37	213	3e-29	0.19	-1202.08		T-CELL SURFACE GLYCOPROTEIN CD4, CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN, IMMUNOGLOBULIN FOLD,

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Pat Blast	Verify score	PMF score	SEQIDOL D score	Compound	PDB annotation
										TRANSMEMBRANE, GLYCOPROTEIN T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
994	1e66	A	1	308	3e-55			102.00	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
994	1e66	A	22	304	3e-55	0.30	-1202.08		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
994	1e66	A	2	307	9.8e-48	0.10	-1202.08		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
994	1e66	C	127	306	9.8e-46	0.16	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGF, PGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1e66	C	19	229	4.2e-29			63.89	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGF, PGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1e66	C	217	337	7e-23	0.10	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGF, PGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1e66	D	127	306	9.8e-44	0.13	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGF, PGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQEOL D score	Compound	PDB annotation
									FACTOR RECEPTOR 1; CHAIN: C, D;	SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1evs	D	19	213	1.3e-29			73.52	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FOR PDGR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1evs	D	217	337	7e-23	0.18	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FOR PDGR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
								63.72	CHIMERIC GERMALINE PRECURSOR OF OXY-COPE CHAIN: L; CHIMERIC GERMALINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNE SYSTEM
994	1d5f	L	28	231	1.4e-12					
994	1d5f	R	8	304	7.5e-48			75.13	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PRR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
994	1eaj	A	36	127	3e-14	0.22	-1202.08		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR COXSACKIEVIRUS B-ADENOVIRUS RECEPTOR, HCAR, VIRUS/VIRAL PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pd Blast	Verify score	PMF score	SEQ/FOI D score	Compound	PDB annotation
994	1epf	A	130	298	9e-30	0.21	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	RECEPTOR, IMMUNOGLOBULIN V DOMAIN FOLD, 2 SYMMETRIC DIMER
994	1epf	A	135	290	7e-22	0.19	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
994	1epf	A	29	213	1.1e-34			82.22	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
994	1epf	A	37	213	1.1e-34	0.28	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
994	1ev2	E	20	213	6e-29			71.72	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, FGFR2, IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOIL FOLD
994	1ev2	G	128	310	4.2e-44	0.22	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, FGFR2, IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOIL FOLD
994	1ev2	G	20	217	3e-30			70.77	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, FGFR2, IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOIL FOLD
994	1ev2	G	30	217	3e-30	0.02	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, FGFR2, IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOIL FOLD

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pat Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									FACTOR 2; CHAIN: A, B; C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: F, G, H	FACTOR RECEPTOR FG2; FG22; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOLD FOLD
994	1evr	C	19	213	9-86-30			76.08	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FG1; FG11; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOLD FOLD
994	1l2q	A	129	307	1-56-32	0.18	-1202.08		HIGH AFFINITY IMAMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM Fc-EPSILON R1-ALPHA; IMAMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
994	1f6a	A	125	307	1-56-37	0.19	-1202.08		HIGH AFFINITY IMAMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-Fc RECEPTOR, Fc(EPSILON) IGE-Fc; IMAMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-Fc
994	1b97	A	128	315	96-37			78.34	JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMAMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
994	1b97	A	129	304	96-37	0.17	-1202.08		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMAMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
994	1b97	A	136	301	1-46-28	0.19	-1202.08		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMAMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
994	1f97	A	31	203	8.4e-29	0.05	-1202.08		JUNCTION ADHESION MOLECULE, CHAIN: A <sub>1</sub>	CELL ADHESION IMAMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
994	1f6g	A	128	304	6e-35	0.07	-1202.08		FC RECEPTOR, FC(GAMMA)RIIA; CHAIN: A <sub>1</sub>	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32, FC RECEPTOR, IMAMUNOGLOBULIN, LEUKOCYTE, CD32
994	1f6g	A	25	215	1.5e-24			64.84	FC RECEPTOR, FC(GAMMA)RIIA; CHAIN: A <sub>1</sub>	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32, FC RECEPTOR, IMAMUNOGLOBULIN, LEUKOCYTE, CD32
994	1f6g	A	37	214	1.5e-24	0.13	-1202.08		FC RECEPTOR, FC(GAMMA)RIIA; CHAIN: A <sub>1</sub>	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32, FC RECEPTOR, IMAMUNOGLOBULIN, LEUKOCYTE, CD32
994	1f6l	A	125	309	3e-36	0.11	-1202.08		LOW AFFINITY IMAMUNOGLOBULIN GAMMA FC REGION CHAIN: A <sub>1</sub>	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMAMUNOGLOBULIN-LIKE, RECEPTOR
994	1f6k	B	28	215	1.1e-10			64.25	MAJOR POLLEN ALLERGEN BET V I-A <sub>1</sub> ; CHAIN: A, D, G, E; IMAMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, E, H, K; ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F, L <sub>1</sub>	IMMUNE SYSTEM BET V I-A <sub>1</sub> , BET V ALLERGEN, BV16 FAB-FRAGMENT, KAPPA MOPC21 CODING SEQUENCE, HEAVY CHAIN OF THE MONOCLONAL ANTIBODY M6T2, BET V I, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX
994	1g9m	L	28	232	1.4e-11			64.69	ENVELOPE GLYCOPROTEIN GP120; CHAIN: G, T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: C; ANTIBODY	VIRUS/VIRAL PROTEIN COMPLEX HIV ENVELOPE PROTEIN/CD4/FAB, HIV-1 EXTERIOR 2 ENVELOPE GP120 FROM LABORATORY-ADAPTED ISOLATE, HBQ2, 3 SURFACE T-

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Dist Blast	Verify score	PMF score	SRGROL D score	Compound	PDB annotation
									17B, LIGHT CHAIN; CHAIN: L; ANTIBODY 17B, HEAVY CHAIN; CHAIN: H; MUTANT AL2 6E7SG; CHAIN: A;	CELL GLYCOPROTEIN CD4, ANTIGEN-BINDING FRAGMENT 4 OF HUMAN IMMUNOGLOBULIN 17B
994	1b8n	A	27	245	14e-10			64.09	NEURAL CELL ADHESION MOLECULE; CHAIN: A;	CELL ADHESION N-CAM; INTERMEDIATE
994	1ie5	A	19	128	2.8e-15	0.15	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A;	IMMUNOGLOBULIN FOLD
994	1ie5	A	207	304	1.3e-22	0.22	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A;	CELL ADHESION N-CAM; INTERMEDIATE
994	1ihl	G	128	310	1.1e-44	0.08	-1202.08		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	IMMUNOGLOBULIN FOLD
994	1ihl	G	30	217	7.5e-28	0.07	-1202.08		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREPOL
994	1hb	B	30	309	1.5e-48			72.20	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE
994	1kca		26	126	4.2e-12	0.09	-1202.08		TWITCHIN CHAIN;	GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR) KINASE KINASE, TWITCHIN,



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pd Blast	Verify score	PMF score	SROFOL D score	Compound	PDB annotation
994	Incl		30	126	1.3e-14	0.03	-1202.08		NULL; TTTN; CHAIN: NULL;	INTRASTERIC REGULATION MUSCLE PROTEIN CONNECTIN, NEXTIN5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
994	Incl		129	301	3e-27	0.29	-1202.08		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL, 2 RECEPTORS, IMMUNOGLOBULIN FOLD
994	Incl		30	126	1.3e-14	0.19	-1202.08		MUSCLE PROTEIN TTN MODULE M5 (CONNECTIN) ITNM3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM4 ITNM58	
994	Zdlf	A	128	301	1.5e-28	0.06	-1202.08		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
994	Zfcb	A	128	307	3e-35	0.10	-1202.08		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
994	Zfcb	A	25	217	1.5e-25			67.36	FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
994	Zfct	A	28	233	4.2e-12			64.42	METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A, C, METAL	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL ID score	Compound	PDB annotation
994	3hm	H	28	215	4.2e-10			65.01	CHIELATASE CATALYTIC ANTIBODY; CHAIN: B, D	IMMUNE 2 SYSTEM
									COMPLEX/ANTIBODY-ANTIGEN) IG*G1 FAB FRAGMENT (HV/HEL5-10) AND LYSOZYME (E.C.3.2.1.17) 3HFM 4 COMPLEX 3HFM 5	
995	1c1g	A	1	245	1.3e-25			61.11	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
995	1c1e		30	177	2.8e-35	0.52	-1202.08		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1
995	1c1e		30	177	7.5e-40			91.26	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1
995	1c1e		32	177	7.5e-40	0.74	-1202.08		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1
995	1j12	J	1	132	2.8e-46			114.02	23S RNA; CHAIN: 0, 5S RNA; CHAIN: 9; RIBOSOMAL PROTEIN 12; CHAIN: A;	RIBOSOME 50S RIBOSOMAL PROTEIN 12P; HMA12, H14; 50S RIBOSOMAL PROTEIN 12P; HMA13, H14; 50S RIBOSOMAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PSI Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
									RIBOSOMAL PROTEIN L3; CHAIN: B;	PROTEIN L4E; HMA14; HL6; 50S RIBOSOMAL PROTEIN L5P; HMA15; HL13; 50S RIBOSOMAL PROTEIN L6P; HMA16; HL10; 50S RIBOSOMAL PROTEIN H86; 50S RIBOSOMAL PROTEIN P6; HMA110; 110S; 50S RIBOSOMAL PROTEIN L13P; HMA113; 50S RIBOSOMAL PROTEIN L14P; HMA114; HL27; 50S RIBOSOMAL PROTEIN L15P; HMA115; HL9; 50S RIBOSOMAL PROTEIN L18P; HMA118; HL12; 50S RIBOSOMAL PROTEIN L18E; HL29; L19; 50S RIBOSOMAL PROTEIN L19E; HMA119; HL24; 50S RIBOSOMAL PROTEIN L21E; HL31; 50S RIBOSOMAL PROTEIN L22P; HMA122; HL23; 50S RIBOSOMAL PROTEIN L23P; HMA123; HL25; L21; 50S RIBOSOMAL PROTEIN L24P; HMA124; HL16; HL15; 50S RIBOSOMAL PROTEIN L24E; HL21/HL22; 50S RIBOSOMAL PROTEIN L29P; HMA129; HL33; 50S RIBOSOMAL PROTEIN L30P; HMA130; HL20; HL16; 50S RIBOSOMAL PROTEIN L31E; L34; HL36; 50S RIBOSOMAL PROTEIN L32E; HL5; 50S RIBOSOMAL PROTEIN L37E; L35E; 50S RIBOSOMAL PROTEIN L39E; HL39E; HL46E; 50S RIBOSOMAL PROTEIN L44E; LA; HL A RIBOSOME ASSEMBLY; RNA-
									RIBOSOMAL PROTEIN L4; CHAIN: C;	
									RIBOSOMAL PROTEIN L5; CHAIN: D;	
									RIBOSOMAL PROTEIN L6; CHAIN: E;	
									RIBOSOMAL PROTEIN L7AE; CHAIN: F;	
									RIBOSOMAL PROTEIN L16; CHAIN: G;	
									RIBOSOMAL PROTEIN L10E; CHAIN: H;	
									RIBOSOMAL PROTEIN L13; CHAIN: I;	
									RIBOSOMAL PROTEIN L14; CHAIN: J;	
									RIBOSOMAL PROTEIN L15; CHAIN: K;	
									RIBOSOMAL PROTEIN L15E; CHAIN: L;	
									RIBOSOMAL PROTEIN L18; CHAIN: M;	
									RIBOSOMAL PROTEIN L18E; CHAIN: N;	
									RIBOSOMAL PROTEIN L19E; CHAIN: O;	
									RIBOSOMAL PROTEIN L21E; CHAIN: P;	
									RIBOSOMAL PROTEIN L22; CHAIN: Q;	
									RIBOSOMAL PROTEIN L23; CHAIN: R;	

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Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									124: CHAIN: S; RIBOSOMAL PROTEIN 124E: CHAIN: T; RIBOSOMAL PROTEIN 129: CHAIN: U; RIBOSOMAL PROTEIN 130: CHAIN: V; RIBOSOMAL PROTEIN 131E: CHAIN: W; RIBOSOMAL PROTEIN 132E: CHAIN: X; RIBOSOMAL PROTEIN 137AE: CHAIN: Y; RIBOSOMAL PROTEIN 137E: CHAIN: Z; RIBOSOMAL PROTEIN 139B: CHAIN: 1; RIBOSOMAL PROTEIN 144E: CHAIN: 2; VES V 5; CHAIN: A <sub>1</sub>	RNA, PROTEIN-RNA, PROTEIN-PROTEIN
995	1qpx	A	1	177	1.3e-39	0.37	-1202.08		VES V 5; CHAIN: A <sub>1</sub>	ALLERGEN ANTIGEN 5; ANTIGEN 5; ALLERGEN, VESPID VENOM
995	1whl		12	132	4.2e-52			71.98	RIBOSOMAL PROTEIN L14; CHAIN: NULL <sub>1</sub>	RIBOSOMAL PROTEIN RIBOSOMAL PROTEIN, RNA-BINDING
996	1c86	A	55	417	2.8e-46			79.13	AXONIN-1; CHAIN: A <sub>1</sub>	CELL ADHESION NEURAL CELL ADHESION
996	1f2q	A	58	225	9.8e-36			140.65	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A <sub>1</sub>	IMMUNE SYSTEM FC-EPSILON R <sub>1</sub> -ALPHA; IMMUNOGLOBULIN FOLD; GLYCOPROTEIN; RECEPTOR, IGE-BINDING 2 PROTEIN
996	1f6a	A	56	225	4.2e-36			141.95	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A <sub>1</sub> IGE EPSILON	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD; GLYCOPROTEIN

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	PSI Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
996	1leg	A	55	224	14c-36			135.32	CHAIN C REGION; CHAIN: B, D; FC RECEPTOR FC(GAMMA)RLA; CHAIN: A;	RECEPTOR, IGF-BINDING 2 PROTEIN, IGF ANTIBODY, IGF-FC IMMUNE SYSTEM, MEMBRANE PROTEIN CD32, FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
996	1hl	A	54	229	7c-34			127.96	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
996	1qpx	A	1	180	9.8c-46			89.64	VES V 5; CHAIN: A;	ALLERGEN ANTIGEN 5; ANTIGEN 5, ALLERGEN, VESPID VENOM
996	26cb	A	55	226	2.8c-38			135.92	FC GAMMA RLB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
999	1bys	A	1	271	1.3c-59			81.76	C-TERMINAL SRC KINASE, CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
999	1csh	A	2	476	14c-87			148.05	GUANOSINE PENTAPHOSPHATE SYNTHETASE, CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP 2 DIPHOSPHOTRANSFERASE, RNA PROCESSING, RNA DEGRADATION
999	1csh	A	9	474	14c-87	0.11	-1202.08		GUANOSINE PENTAPHOSPHATE SYNTHETASE, CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP 2

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	EVD AA	P4 Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
999	1ejp	A	2	476	1.4e-87			140.99	GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	DIPHOSPHOTRANSFERASE, RNA PROCESSING, RNA DEGRADATION
999	1ejp	A	9	474	1.4e-87	0.17	-1202.08		GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP DIPHOSPHOTRANSFERASE, 2 RNA PROCESSING, RNA DEGRADATION
999	1ejf	A	12	344	2.8e-39			82.19	TRANSCRIPTIONAL REPRESSOR TDP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
999	1fgk	A	4	271	1.3e-55			101.99	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K; FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2
999	1fgk	B	2	271	2.8e-56			99.67	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE PHOSPHOTRANSFERASE FGFR1K; FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE,

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
999	1gct	B	5	343	2.8e-51			75.43	GT-ALPHA/GT-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
999	1lep	A	1	271	5.6e-74			115.77	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A; B;	BINDING (TRANSDUCER) BETA.1, TRANSDUCIN BETA SUBUNIT; GAMMA.1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
999	1lf3	A	1	271	1.3e-55			90.03	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	TRANSFERRASE (SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSDUCER/SUBSTRATE)
999	1lqe	A	3	270	9.8e-77			105.38	LCK KINASE; CHAIN: A;	TRANSFERRASE ALPHA BETA FOLD
1000	1ain	A	17	117	9.8e-45	0.69	-1202.08		B*3501; CHAIN: A; B; PEPTIDE VPLRPMVY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC H.1.A, H.1.A-B*3501, H1Y.2, NFE, COMPLEX (ANTIGEN/PEPTIDE)
1000	1afa	B	22	115	2.8e-39	0.54	-1202.08		HLA-DRE3; CHAIN: A; B; CLIP; CHAIN: C;	COMPLEX (TRANSMEMBRANE/GELCO PROTEIN) MHC GLYCOPROTEIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1000	1agd	A	17	117	4.2c-44	0.36	-1202.08		B*0801: CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKSKYRL-INDEX PEPTIDE); CHAIN: C;	COMPLEX TRANSMEMBRANE/GLYCOPROTEIN
1000	1agd	B	22	115	2.8c-39	0.78	-1202.08		HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, I, K; HLA-A2; CHAIN: C, F, L, E;	COMPLEX (MHC PROTEIN/ANTIGEN) DR A, DR B1 01010; COMPLEX (MHC PROTEIN/ANTIGEN); HISTOCOMPATIBILITY ANTIGEN
1000	1agx	A	17	118	1.4c-44	0.54	-1202.08		HLA-GW3 (HEAVY CHAIN); CHAIN: A;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1000	1agx	B	1	85	7c-32			129.28	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID PROTEIN; CHAIN: P;	IMMUNE SYSTEM SEV9; MAJOR HISTOCOMPATIBILITY COMPLEX PEPTIDE-MHC
1000	1agx	B	21	119	1.4c-35			166.40	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN:	IMMUNE SYSTEM SEV9; MAJOR HISTOCOMPATIBILITY COMPLEX PEPTIDE-MHC



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
									A; BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID PROTEIN; CHAIN: P; HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHS.A.3 / ILSA-B/ASTERISK27055 IHS.A.4	
1000	Ihsa	A	17	117	9.8e-45	0.39	-1202.08		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHS.A.3 / ILSA-B/ASTERISK27055 IHS.A.4	
1000	Ilf4f	A	17	116	8.4e-42	0.46	-1202.08		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C; MHC CLASS II ILSA-DO8; CHAIN: A; MHC CLASS II ILSA-DO8; CHAIN: B; INSULIN B PEPTIDE; CHAIN: C	IMMUNE SYSTEM MA6-4 ANTIGEN: MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1000	Ijhs	B	22	115	2.8e-40	0.24	-1202.08		MHC CLASS II ILSA-DO8; CHAIN: A; MHC CLASS II ILSA-DO8; CHAIN: B; INSULIN B PEPTIDE; CHAIN: C	IMMUNE SYSTEM ILSA-DO8, INSULIN B PEPTIDE, TYPE I DIABETES, AUTOMATIVITY
1000	Imlh	A	17	115	8.4e-40	0.60	-1202.08		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE (YMARPTVIL) CHAIN: F; Q; HISTOCOMPATIBILITY	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL, CHAIN: MHC-E, HLA-E, MHC CLASS ILSA-E, HLA-E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, ILSA, 2 BETA 2 MICROGLOBULIN PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC IMMUNE SYSTEM
1000	Iqgd	A	17	115	1.3e-42	0.65	-1202.08		HISTOCOMPATIBILITY	IMMUNE SYSTEM

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									LEUKOCYTE ANTIGEN (HLA-CW4 CHAIN: A <sub>1</sub> BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (G)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1000	3ftu	B	1	85	5.6e-32			120.95	NEONATAL FC RECEPTOR; CHAIN: A, C <sub>1</sub> E, BETA-2- MICROGLOBULIN; CHAIN: B, D, F;	FCRN, BRAMBLELL RECEPTOR; COMPLEX (IMMUNOGLOBULIN/BINDING PROTEIN)
1000	3ftu	B	21	119	1.4e-35			157.46	NEONATAL FC RECEPTOR; CHAIN: A, C <sub>1</sub> E, BETA-2- MICROGLOBULIN; CHAIN: B, D, F;	FCRN, BRAMBLELL RECEPTOR; COMPLEX (IMMUNOGLOBULIN/BINDING PROTEIN)
1007	1a7i		390	443	5.1e-15	0.43	0.58		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC2 FINGER
1007	1a7i		390	447	5.6e-10	0.17	0.66		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC2 FINGER
1007	1a7i		448	507	5.6e-14	-0.10	0.57		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC2 FINGER
1007	1a7i		449	506	1.7e-16	0.08	0.58		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEINS, METAL-BINDING PROTEIN, ZINC2 FINGER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pa Blast	Verify score	PMF score	SEQIDOL D score	Compound	PDB annotation
1007	1a7i		510	575	34e-12	-0.05	0.30		QCRP2 (LIM); CHAIN: NULL;	BINDING PROTEIN, ZINC 2 FINGER
1007	1a7i		510	577	9.8e-10	0.38	0.76		QCRP2 (LIM); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1007	1b8t	A	383	572	1.2e-33	-0.26	0.03		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1007	1b8t	A	449	577	8.4e-26	0.06	0.07		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1007	1cdl		382	443	1.7e-16	-0.38	0.33		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS
1007	1cdl		382	449	2.8e-13	-0.54	0.18		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS
1007	1cdl		446	502	6.8e-14	-0.12	0.51		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS
1007	1cdl		450	516	7e-16	-0.26	0.05		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS
1007	1cdl		508	572	1.5e-13	-0.11	0.48		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMR score	SEOPOL D score	Compound	PDB annotation
1007	1cdl		510	577	2.8e-12	0.16	0.55		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	ICTL 15 METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS
1007	1ccx	A	388	443	8.5e-16	0.52	0.68		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2, CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1007	1ccx	A	388	446	4.2e-12	0.26	0.19		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2, CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1007	1ccx	A	448	504	1.4e-14	0.45	0.78		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2, CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1007	1ccx	A	507	572	8.5e-14	-0.05	0.25		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2, CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1007	1ccx	A	507	574	9.8e-12	-0.37	0.89		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2, CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1007	1g47	A	381	450	2.8e-14	0.05	0.00		PINCH PROTEIN; CHAIN: A;	CELL ADHESION PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN; LIM DOMAIN; ZN FINGER
1007	1g47	A	510	577	1.4e-07	0.53	-0.09		PINCH PROTEIN; CHAIN: A;	CELL ADHESION PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN; LIM DOMAIN; ZN FINGER
1007	1iml		388	449	5.6e-12	0.37	0.57		CYSTEINE RICH INTERSTITIAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRP2, METAL-BINDING PROTEIN, LIM DOMAIN
1007	1iml		390	461	3.4e-16	-0.02	0.57		CYSTEINE RICH INTERSTITIAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRP2, METAL-BINDING PROTEIN, LIM DOMAIN
1007	1iml		449	512	1.4e-14	0.24	0.00		CYSTEINE RICH	METAL-BINDING PROTEIN CRP2, METAL-BINDING PROTEIN, LIM DOMAIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1007	1iml		449	513	5.1e-16	0.01	0.47		INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1007	1iml		508	577	5.6e-12	0.07	1.00		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1007	1zfo		508	541	0.00056	-0.34	0.15		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL; LASP-I; CHAIN: NULL;	METAL-BINDING PROTEIN CRP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1012	1a88	A	2	149	4.2e-27	0.54	0.00		CHLOROPEXOXIDASE L; CHAIN: A, B, C;	HALOPEXOXIDASE BROMOPEXOXIDASE L, HALOPEXOXIDASE L, HALOPEXOXIDASE L, HALOPEXOXIDASE, OXIDOREDUCTASE
1012	1a8q		2	156	4.2e-24	0.36	-0.07		BROMOPEXOXIDASE A1; CHAIN: NULL;	HALOPEXOXIDASE CELLOPEXOXIDASE A1, HALOPEXOXIDASE A1; HALOPEXOXIDASE, OXIDOREDUCTASE
1012	1a8s		2	149	1.4e-26	0.53	0.39		CHLOROPEXOXIDASE F; CHAIN: NULL;	HALOPEXOXIDASE HALOPEXOXIDASE F, HALOPEXOXIDASE F, OXIDOREDUCTASE, PROPIONATE COMPLEX
1012	1aao	A	13	213	1.4e-24	0.45	1.00		CARBOXYLESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE HYDROLASE HYDROLASE
1012	1aao	A	13	229	1.8e-43	0.70	1.00		CARBOXYLESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE HYDROLASE HYDROLASE
1012	1aao	A	13	229	5.1e-31	0.53	1.00		CARBOXYLESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE HYDROLASE HYDROLASE
1012	1aao	A	8	214	1.4e-24			106.42	CARBOXYLESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE HYDROLASE HYDROLASE

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Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	PI Blast	Verify score	PMF score	SEOTOL D score	Compound	PDB annotation
1012	1ano	A	8	230	1.8e-43			123.46	CARBOXYL ESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE
1012	1b6g		6	192	7e-19	0.02	0.09		HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1012	1bm6	A	6	146	5.6e-22	0.18	0.62		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE DEHALOGENASE, ALPHA/BETA-HYDROLASE, DEHA, CRYSTAL STRUCTURE
1012	1cdx	A	9	157	8.4e-21	0.44	0.62		2-HYDROXY-6-OXO-6- PHENYLHEXA-2,4- DIENOATE CHAIN: A;	HYDROLASE PHB, HYDROLASE, PCB DEGRADATION
1012	1cfj	A	7	198	3.4e-31	0.24	-0.07		PARA-NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PHB ESTERASE; DIRECTED EVOLUTION, ORGANIC ACTIVITY, 2 PHB ESTERASE
1012	1ev2	A	12	144	2.8e-15	0.24	-0.05		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE LINB, 1,3,4,6- TETRACHLORO-1,4- CYCLOHEXADIENE DEHALOGENASE, LINDANE, BIODEGRADATION,
1012	1evl		18	128	5.6e-09	0.60	0.19		TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL- HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
1012	1dm		5	199	7e-27	0.59	0.94		DIBENYLACTONE HYDROLASE; CHAIN: NULL;	HYDROLASE ENZYME DLH; DIENYLACTONE HYDROLASE, AROMATIC HYDROCARBON CATALYSIS, 2 SERINE ESTERASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1012	1dgz	A	96	215	0.00034	0.31	0.71		ANTIGEN 85-C; CHAIN: A, B;	CARBOXYMETHYLENETHENOL DASE, 3 HYDROXYLIC ENZYME
1012	1eas	A	3	223	1.7e-36	0.22	0.37		ACETYLCHOLINESTERASE; CHAIN: A;	IMADINE SYSTEM 55C ANTIGEN, 85C MYOBRACETININ
1012	1ebv	A	13	172	1.4e-20	0.53	0.16		SOLUBLE EPOXIDE HYDROLASE; CHAIN: A, B, C, D;	TUBERCULOSIS, FIBRONECTIN CHOLINESTERASE SERINE HYDROLASE, NEUROTANSAMATTER
1012	1ek1	A	2	149	2.8e-25	0.51	0.48		EPOXIDE HYDROLASE; CHAIN: A, B;	CLEAVAGE, CATALYTIC 2 TRIAD, ALPHA/BETA HYDROLASE
1012	1ek1	A	2	149	2.8e-25	0.51	0.48		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HYDROLASE, ALPHA/BETA HYDROLASE FOLD, EPOXIDE DEGRADATION, 2 EPICHLOROHYDRIN
1012	1ek1	B	2	149	2.8e-25	0.64	0.55		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1012	1ekh	A	25	167	0.00014	0.52	0.03		TRIACYLGLYCEROL ACYL-HYDROLASE; CHAIN: A, C, COLIPASE; CHAIN: B, D	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1012	16w	A	2	222	5.1e-34	0.33	-0.08		BILE SALT ACTIVATED LIPASE; CHAIN: A;	COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION
1012	1f52	A	13	214	7e-32	0.84	1.00		ACYL PROTEIN THIOESTERASE I; CHAIN: A, B;	HYDROLASE BILE SALT ACTIVATED LIPASE, ESTERASE, CATALYTIC DOMAIN
1012	1f52	A	13	214	7e-32	0.84	1.00		ACYL PROTEIN THIOESTERASE I; CHAIN: A, B;	HYDROLASE ALPHA/BETA HYDROLASE, SERINE HYDROLASE, SAD, ANOMALOUS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1012	1q2	A	13	231	3.4e-38	0.52	1.00		ACYL PROTEIN THIOESTERASE 1; CHAIN: A, B;	2 DIFFRACTION HYDROLASE ALPHA/BETA HYDROLASE, SERINE HYDROLASE, SAD, ANOMALOUS 2 DIFFRACTION
1012	1q2	A	1	215	7e-32			116.80	ACYL PROTEIN THIOESTERASE 1; CHAIN: A, B;	HYDROLASE ALPHA/BETA HYDROLASE, SERINE HYDROLASE, SAD, ANOMALOUS 2 DIFFRACTION
1012	1grl		25	167	0.00014	0.39	0.11		RP2 LIPASE; CHAIN: NULL;	SERINE ESTERASE RELATED PROTEIN 2 LIPASE, SERINE ESTERASE, HYDROLASE, LIPID DEGRADATION, PANCREAS, 2 GLYCOPROTEIN, CHIMERIC HYDROLASE
1012	1l6w	A	23	166	8.4e-09	0.19	0.21		LIPASE A; CHAIN: A, B;	HYDROLASE HYDROLASE ALPHA/BETA
1012	1l6m	A	5	157	7e-12	0.39	0.00		BREFFELDIN A ESTERASE; CHAIN: A, B;	SERINE HYDROLASE, SERINE HYDROLASE, DEGRADATION OF BREFFELDIN A, ALPHA/BETA 2 HYDROLASE FAMILY
1012	1lpb	B	25	167	5.6e-05	0.25	0.04		HYDROLASE/CARBOXY LIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
1012	1lma	A	3	221	5.1e-36	0.30	0.46		ACETYLCOLINESTERASE SE; CHAIN: A, B, C, D;	HYDROLASE MACHIE: HYDROLASE, SERINE ESTERASE, ACETYLCOLINESTERASE, TETRAMER, 2 HYDROLASE FOLD,



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOI, D score	Compound	PDB annotation
1012	1qg3	A	7	198	3.4e-31	0.09	-0.07		PARA-NITROBENZYL ESTERASE; CHAIN: A;	GLYCOSYLATED PROTEIN, HYDROLASE PNB ESTERASE, ALPHA, BETA, HYDROLASE DIRECTED EVOLUTION
1012	1qg2	D	18	128	5.6e-09	0.46	0.30		TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	HYDROLASE PSEUDOMONADACEAE, CIS-PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
1012	1qg4	A	25	159	5.6e-09	0.23	-0.05		HYDROXYNITRILE LYASE; CHAIN: A;	LYASE OXYNITRILE LYASE; OXYNITRILE, CYANOGENESIS, CYANHYDRIN FORMATION, LYASE
1012	1qtr	A	1	130	2.8e-13	0.32	-0.02		PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA, HYDROLASE ROLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERPANTIN, AMINOPEPTIDASE
1012	1thg		3	204	8.5e-30	0.05	0.07		HYDROLASE(CARBOXY LIC ESTERASE) LIPASE (E.C.3.1.1.3) TRIACYLGLYCEROL HYDROLASE 1THG.3	
1012	2hcc		2	216	3.4e-35	0.32	-0.08		CHOLESTEROL ESTERASE; CHAIN: NULL;	HYDROLASE BILE SALT ACTIVATED LIPASE, BILE SALT STIMULATED HYDROLASE, SERINE ESTERASE, LIPASE
1012	4hlp	D	18	128	1.4e-09	0.35	0.13		TRIACYL-GLYCEROL-HYDROLASE; CHAIN: D, E;	LIPASE LIPASE, LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIOL YCERIDE ANALOCOD, ENANTIOSELECTIVITY
1017	1aih	A	211	293	1.2e-24	-0.05	1.00		QGRS ZINC FINGER PEPTIDE; CHAIN: A;	COMPLEX (ZINC FINGERDNA) COMPLEX (ZINC FINGERDNA)

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Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pat Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	239	319	2.8e-29	-0.41	1.00		QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	239	348	5.1e-23	-0.37	0.51		QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	463	543	3.4e-42	0.10	1.00		QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	58	140	1.4e-25			77.51	QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	72	154	1.4e-27			54.94	QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	87	154	2.8e-31			57.17	QGRS ZINC FINGER	COMPLEX (ZINC FINGER/DNA)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PEPTIDE, CHAIN: A; DUPLICATION; BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1ah	A	90	169	1.1e-23	-0.34	0.00		QGR ZINC FINGER PEPTIDE, CHAIN: A; DUPLICATION; OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
									DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE
1017	Imey	C	116	198	2.8e-39	-0.24	0.17		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE
									DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE
1017	Imey	C	172	263	7e-43	-0.07	0.92		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE
									DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE
1017	Imey	C	210	291	9.8e-47	-0.07	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE
									DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE
1017	Imey	C	238	319	2.8e-47	-0.33	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE
									DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE
1017	Imey	C	266	347	8.4e-48	-0.03	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE

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Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
1017	1mey	C	294	375	1.3e-48	0.16	0.98		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mey	C	29	111	2.8e-50			98.30	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mey	C	322	403	8.4e-50	0.63	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mey	C	350	431	2.8e-50	0.22	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mey	C	378	459	7e-51	0.23	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mey	C	406	487	5.6e-50	0.27	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mey	C	434	515	1.1e-49	0.09	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN,

Table 5

SEQ ID	PDB ID	CHAIN ID	STAR TAA	END AA	Pal Blast	Verify score	PMF score	SEQUAL D score	Compound	PDB annotation
1017	Inney	C	462	543	42e-50	0.16	1.00		CHAIN: C, F, G; DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1017	Inney	C	462	544	42e-50			102.09	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1017	Inney	C	490	565	14e-43	0.07	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1017	Inney	C	57	139	2.8e-50			100.99	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1017	Inney	C	71	153	2.8e-50			69.61	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1017	Inney	C	86	154	4.2e-50			76.26	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1017	Inney	C	88	169	1.4e-37	-0.48	0.15		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

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Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
									FINGER PROTEIN; CHAIN: C, F, G.	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mev	G	114	141	1.4e-09	-0.61	0.01		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G.	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mev	G	208	235	2.8e-11	0.29	0.63		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G.	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mev	G	264	291	4.2e-12	-0.13	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G.	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1lf3	A	173	259	4.2e-17	-0.08	0.11		TRANSCRIPTION FACTOR IIA; CHAIN: A, 5S RNA GENE; CHAIN: E, F.	COMPLEX (TRANSCRIPTION REGULATION/DNA) TEIIA; 5S GENE; NMR, TEIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1017	1lf6	A	147	403	1.4e-49	-0.57	0.03		TEIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F.	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1lf6	A	173	328	2.8e-34	-0.35	0.04		TEIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE.	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Pd Blast	Verify score	PMF score	SEQ/POU. D score	Compound	PDB annotation
1017	1t66	A	1	153	1.4e-36			90.49	CHAIN: B, C, E, F; TH1UA, CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA, RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1t66	A	211	431	3.4e-55	-0.47	0.21		TH1UA, CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1t66	A	267	412	4.2e-38	0.01	0.90		TH1UA, CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1t66	A	2	153	4.2e-37			91.96	TH1UA, CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1t66	A	323	487	3.4e-68	-0.14	0.76		TH1UA, CHAIN: A, D, S5 RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pst Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA) RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tf6	A	350	520	6.8e-72			108.86	TFIIIA, CHAIN: A, D, 5S RIBOSOMAL RNA GENE, CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tf6	A	351	496	2.8e-39	0.13	1.00		TFIIIA, CHAIN: A, D, 5S RIBOSOMAL RNA GENE, CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tf6	A	379	543	6.8e-72	-0.19	1.00		TFIIIA, CHAIN: A, D, 5S RIBOSOMAL RNA GENE, CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tf6	A	407	551	2.8e-38	-0.00	0.99		TFIIIA, CHAIN: A, D, 5S RIBOSOMAL RNA GENE, CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tf6	A	435	565	1.4e-32	0.08	1.00		TFIIIA, CHAIN: A, D, 5S RIBOSOMAL RNA GENE,	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1017	1tf6	A	7	154	8.4e-37			68.08	TH1UA; CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tf6	A							TH1UA; CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tf6	A	89	249	8.4e-31	0.13	0.24		TH1UA; CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1ubd	C	124	235	1.4e-27	-0.45	0.07		YY1; CHAIN: G, ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	180	291	2.8e-30	-0.19	0.80		YY1; CHAIN: G, ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
1017	1ubd	C	1	111	2.8e-35			89.38	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	237	375	3.4e-36	-0.42	0.81		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	246	347	9.8e-34	-0.24	0.90		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	265	403	3.4e-47	-0.33	0.62		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	33	140	4.2e-36			66.22	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

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Table 5

Seq ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SeqPOL D score	Compound	PDB annotation
1017	1ubd	C	348	460	6.8e-53	-0.08	1.00		Y11; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	INITIATOR ELEMENT, Y11, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1017	1ubd	C	3	111	1.4e-36			82.90	Y11; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATON(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, Y11, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1017	1ubd	C	433	544	1.7e-51	0.11	1.00		Y11; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATON(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, Y11, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1017	1ubd	C	439	543	4.2e-35	0.01	1.00		Y11; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATON(DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, Y11, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1017	1ubd	C	467	563	3,46-45	0.02	0.83		YY1: CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	470	566	2,86-32	0.17	0.96		YY1: CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	2adt		177	238	3,46-12	-0.04	0.19		ADRI: CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1017	2gli	A	144	293	5,66-30	-0.33	0.24		ZINC FINGER PROTEIN GILI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL; GIL, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	177	405	1,56-51	-0.61	0.43		ZINC FINGER PROTEIN GILI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL; GIL, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	1	139	9,86-34			85.51	ZINC FINGER PROTEIN GILI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL; GIL, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	1	140	2,86-33			88.47	ZINC FINGER PROTEIN	COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOPOL D score	Compound	PDB annotation
1017	2gli	A	238	377	1.3e-33	0.18	0.95		GLI1; CHAIN: A; DNA; CHAIN: C; D;	PROTEIN/DNA FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	238	377	1.3e-33	0.18	0.95		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	266	433	3.4e-61	0.07	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	2	141	2.8e-33			59.85	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	330	458	2.8e-35	0.16	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	350	489	1.2e-66	0.19	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	378	544	1e-67	0.13	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	414	545	4.2e-35	0.00	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	442	566	8.4e-33	-0.02	0.87		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Ps Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1017	2gi	A	462	563	1.7e-45	0.30	0.78		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	(DNA-BINDING PROTEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gi	A	5	154	7e-32			62.95	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1020	1a7i		137	194	1.7e-16	0.13	0.99		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1020	1a7i		258	313	5.1e-10	0.37	0.66		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1020	1a7i		9	69	5.6e-13			51.43	QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1020	1b8t	A	138	313	5.1e-29	-0.43	0.15		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1020	1b8t	A	199	313	2.8e-11	-0.05	0.28		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1020	1b8t	A	74	273	1.7e-37			102.41	CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOFOL ID score	Compound	PDB annotation
1020	1b8t	A	76	251	1.7e-37	-0.51	0.57		GRP1, CHAIN: A;	DIFFERENTIATION, CONTRACTILE, CONTRACTILE LIM DOMAIN, GRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1020	1c1l		136	192	1.7e-14	0.19	0.94		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS ICTL 15
1020	1c1l		1	79	2.8e-18			50.28	AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS ICTL 15
1020	1c1l		258	313	3.4e-10	0.69	0.51		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS ICTL 15
1020	1c3x	A	136	194	8.5e-15	0.41	0.81		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2, CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1020	1c3x	A	256	313	1.2e-11	0.71	0.99		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2, CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1020	1c3x	A	8	67	1.3e-16			53.17	CYSTEINE AND GLYCINE-RICH PROTEIN CRP2, CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1020	1c3t	A	46	210	2.8e-07			62.37	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
1020	1g44	C	31	290	0.0068			77.40	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1020	1iml		138	203	5.1e-15	0.20	0.18		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN GRP, METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1020	1k6o		14	182	6.8e-07			69.70	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1020	Imey	C	221	307	5.6e-36	0.03	-0.15		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1024	1a1h	A	350	432	3e-28			78.62	QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1024	Imey	C	17	93	1.1e-46			61.77	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1024	Imey	C	181	262	1.1e-47	0.11	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1024	Imey	C	209	290	4.2e-49	0.23	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1024	Imey	C	21	103	1.4e-50			99.15	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1024	Imey	C	237	318	1.1e-49	0.70	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.



Table 5

SEQ ID NO:	PDB ID	CIAT ID	STAR TAA	END AA	Pst Blast	Verify score	PMF score	SEQPOL ID score	Compound	PDB annotation
1024	Imey	C	293	374	1.4e-50	0.14	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	29	111	1.4e-50			97.98	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	321	402	1.4e-50	0.32	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	349	430	1.4e-50	0.03	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	349	431	1.4e-50			100.76	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	377	438	5.6e-38	0.06	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	3	64	7e-40			59.08	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN,

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pat Blast	Verify score	Pfaff score	SEQFOL D score	Compound	PDB annotation
1024	1t66	A	1	133	76-34			64.03	CHAIN: C, F, G; TFIIIA: CHAIN: A, D, SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F; POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1024	1t66	A	1	144	146-35			95.70	TFIIIA: CHAIN: A, D, SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F; POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1024	1t66	A	265	430	156-70			116.54	TFIIIA: CHAIN: A, D, SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F; POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA), COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1024	1t6d	C	181	291	36-52			83.93	YY1: CHAIN: C, ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1: TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1024	1t6d	C	189	290	146-35	0.16	-1202.08		YY1: CHAIN: C, ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1: TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1024	1ubd	C	1	111	2.8e-36			83.50	YY1: CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1024	1ubd	C	217	318	2.8e-35	0.16	-1202.08		YY1: CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1024	1ubd	C	21	131	1.4e-36			84.44	YY1: CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1024	1ubd	C	235	346	3e-52	0.23	-1202.08		YY1: CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1024	2gli	A	153	292	2.8e-33	0.01	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	REGULATON(DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GIL ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	1	132	1.4e-32			87.11	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GIL ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	1	133	8.4e-32			86.13	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GIL ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	209	348	3e-66	0.17	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GIL ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	217	345	4.2e-35	0.24	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GIL ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	237	376	1.3e-67			98.02	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GIL ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	301	429	7e-35	0.01	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GIL ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1026	1dix	A	1	222	1.5e-05			51.64	SUBSTRATE BINDING DOMAIN OF DNAX; CHAIN: A; SUBSTRATE PEPTIDE (7 RESIDUES); CHAIN: B;	COMPLEX (MOLECULAR GLIARON/PEPTIDE) DNAX; HEAT SHOCK PROTEIN 70 KDA (HS70), COMPLEX 2 (MOLECULAR

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1026	1dky	B	1	206	0.0001			50.66	DNAX; CHAIN: A, B; PEPTIDE SUBSTRATE; CHAIN: C, D;	CHAPERONE/PEPTIDE COMPLEX (MOLECULAR CHAPERONE/PEPTIDE) DNAX; HEAT SHOCK PROTEIN 70 KDA (HSP70); COMPLEX 2 (MOLECULAR CHAPERONE/PEPTIDE)
1029	1aut	L	261	326	0.00024	0.03	0.33		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOTHROMBIN (IIA); HYDROLASE, SERINE PROTEINASE; PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1029	1dva	L	261	326	0.0006	-0.18	0.19		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, L; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1029	1els	A	115	200	7.2e-09	-0.02	0.11		AGGLUTININ	SUGAR BINDING PROTEIN (IDA; LECTIN, HEVEIN DOMAIN, IDA, SUPERANTIGEN)
1029	1els	A	196	270	6e-05	0.15	0.07		AGGLUTININ	SUGAR BINDING PROTEIN (IDA; LECTIN, HEVEIN DOMAIN, IDA, SUPERANTIGEN)
1029	1ext	A	65	227	3e-27	0.00	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMR score	SEOFOL D score	Compound	PDB annotation
1029	1ect	A	98	249	2.4e-14			63.01	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A-B	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
1029	1g40	A	26	268	3e-29			93.82	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B	IMMUNE SYSTEM BETA, MODULE
1029	1g44	A	36	268	3e-28			93.40	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C	IMMUNE SYSTEM BETA, MODULE
1029	1g44	B	42	268	6e-33			90.73	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C	IMMUNE SYSTEM BETA, MODULE
1029	1g44	C	42	277	9e-24			92.61	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C	IMMUNE SYSTEM BETA, MODULE
1029	1k0		22	216	3e-14	0.04	-1292.08		LAMININ; CHAIN: NULL, LAMININ; CHAIN: NULL, FACTOR I;A, CHAIN: C, L, D-PHE-PRO-ARG, CHAIN: I	GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN COAGULATION(INHIBITOR) CHRISTMAS FACTOR, COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1029	1k0		27	199	3e-14			71.49	LAMININ; CHAIN: NULL, FACTOR I;A, CHAIN: C, L, D-PHE-PRO-ARG, CHAIN: I	GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN COAGULATION(INHIBITOR) CHRISTMAS FACTOR, COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1029	1p1x	L	10	144	2.4e-13			64.18	LAMININ; CHAIN: NULL, FACTOR I;A, CHAIN: C, L, D-PHE-PRO-ARG, CHAIN: I	GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN COAGULATION(INHIBITOR) CHRISTMAS FACTOR, COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1029	1qub	A	7	275	3e-30			68.14	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, STIMUL, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1029	9wga	A	93	269	1.5e-30			94.61	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ	

Table 5

SEQ ID No:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1031	1awq	A	2	164	2.8e-91	1.33	-1202.08		(ISOLLECTIN 2) 2WGA.3	COMPLEX (ISOMERASE/PEPTIDE) COMPLEX (ISOMERASE/PEPTIDE), CYCLOPHILIN A, HIV-1 CAPSID, 2 PSEUDO-SYMMETRY
1031	1awq	A	2	165	2.8e-91			269.60	CYCLOPHILIN A, CHAIN: A; PEPTIDE FROM THE HIV-1 CAPSID PROTEIN; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) COMPLEX (ISOMERASE/PEPTIDE), CYCLOPHILIN A, HIV-1 CAPSID, 2 PSEUDO-SYMMETRY
1031	1cdq	A	7	178	2.8e-63			98.08	TRANSFORMING PROTEIN P21H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1035	1alh	A	13	99	2.8e-29			77.80	QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATE OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1035	1alh	A	98	182	8.4e-23	0.31	-1202.08		QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATE OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1035	1mey	C	129	210	2.8e-41	0.38	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
1035	1mey	C	12	94	9.8e-51			95.25	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/FOI D score	Compound	PDB annotation
									FINGER PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	1mey	C	12	98	4.2e-49			94.62	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	1mey	C	157	238	4.2e-44	0.20	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	1mey	C	185	266	2.8e-46	0.09	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	1mey	C	1	67	1.4e-41			73.50	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	1mey	C	213	294	4.2e-48	0.10	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	1mey	C	23	105	9.8e-51			96.53	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	1mey	C	269	350	1.4e-48	0.12	-1202.08		DNA: CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA)



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	297	378	2.8e-49	0.50	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
									DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	325	406	7e-50	0.16	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	353	434	7e-50	0.49	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
									DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	381	462	2.8e-50	0.27	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
									DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	409	490	5.6e-51	0.51	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
									DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	437	518	1.4e-50	0.28	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	PsI Blast	Verify score	PMF score	SEQ/FOL D score	Compound	PDB annotation
1035	Imey	C	465	546	1.3e-50	0.23	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1035	Imey	C	493	574	8.4e-50	0.03	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1035	Imey	C	49	131	1.4e-50			89.69	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1035	Imey	C	6	85	7e-50			90.19	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1035	Imey	C	97	182	9.8e-38	0.42	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1035	Imey	C	98	182	3e-38	0.45	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE.
1035	1H3	A	12	101	4.2e-14			58.28	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E; F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TTHIA: 5S GENE, NMV, TTHIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMR score	SEQPOL D score	Compound	PDB annotation
1035	1t66	A	1	134	8.4e-36			71.45	TFIIIA; CHAIN: A, D, 5S; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1035	1t66	A	1	145	1.4e-35			84.26	TFIIIA; CHAIN: A, D, 5S; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1t66	A	242	387	5.6e-38	0.02	-1202.08		TFIIIA; CHAIN: A, D, 5S; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1t66	A	381	544	4.5e-69			113.05	TFIIIA; CHAIN: A, D, 5S; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1t66	A	410	556	9.8e-39	0.16	-1202.08		TFIIIA; CHAIN: A, D, 5S; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

SEQ NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pst Dist	Verity score	PMF score	SRCFOOL D score	Component	PDB annotation
1035	1u6	A	438	574	1.4e-37	0.07	-1202.08		THE1A; CHAIN: A; D; S5 RIBOSOMAL RNA GENE; CHAIN: B; C; E; F;	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1u6	A	439	574	1e-53	0.16	-1202.08		THE1A; CHAIN: A; D; S5 RIBOSOMAL RNA GENE; CHAIN: B; C; E; F;	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1u6	C	100	210	4.2e-27	0.01	-1202.08		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A; B;	COMPLEX (TRANSCRIPTION REGULATION/DNA YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER, PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1u6	C	12	106	1.4e-29			68.31	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A; B;	COMPLEX (TRANSCRIPTION REGULATION/DNA YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER, PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1u6	C	1	103	4.2e-36			76.28	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG

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Table 5

Seq ID No.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SeqPOL D score	Compound	PDB annotation
1035	1ubd	C	23	133	4.2e-36			83.22	INITIATOR ELEMENT DNA; CHAIN: A, B;	1: TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
									YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1: TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	323	434	4.5e-49	0.40	-1202.08		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1: TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
									YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1: TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	358	462	1.4e-36	0.04	-1202.08		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1: TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
									YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1: TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	417	518	1.4e-36	0.02	-1202.08		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1: TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
									YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1: TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/SOL. D score	Compound	PDB annotation
										RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1035	1ubd	C	435	546	6c-51	0.41	-1202.08		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
										COMPLEX (TRANSCRIPTION) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1035	1ubd	C	463	574	1.5c-49	-0.00	-1202.08		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
										COMPLEX (TRANSCRIPTION) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1035	1ubd	C	67	182	1.5c-37	0.45	-1202.08		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
										COMPLEX (TRANSCRIPTION) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1035	2gfi	A	1	110	1.3c-25			53.64	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
										COMPLEX (DNA-BINDING) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1035	2gfi	A	1	132	4.2c-33			76.13	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
										COMPLEX (DNA-BINDING) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1035	2gli	A	1	134	2.8e-33			82.37	ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	297	436	4.5e-65			98.88	ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	297	492	4.5e-65	0.00	-1202.08		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	333	461	7e-35	0.54	-1202.08		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	353	520	7.5e-64	0.04	-1202.08		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	389	520	2.8e-35	0.13	-1202.08		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	417	545	8.4e-35	0.19	-1202.08		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	459	574	1.2e-61	0.16	-1202.08		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	69	212	1.1e-26	0.07	-1202.08		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1;

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PstF score	SeqPOL D score	Compound	PDB annotation
									CHAIN: C, D;	GIL ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1042	12e8	IE	336	518	5-6e-51	-0.05	0.10		2E8 (GGI-KAPPA-) ANTIBODY; CHAIN: L, H, M, P.	IMMUNOGLOBULIN
1042	1a31	H	336	515	4.2e-50	0.02	0.19		IMMUNOGLOBULIN FAB ALDER, DISFAYORED REACTION, CATALYTIC ANTIBODY, 2	IMMUNOGLOBULIN
1042	1adq	L	51	240	8.4e-32	-0.11	0.18		IGG4 REA; CHAIN: A, RF- AN IGM/LAMBDA; CHAIN: H, L;	IMMUNOGLOBULIN
1042	1afv	H	336	517	5.6e-51	0.17	0.10		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	IMMUNOGLOBULIN
1042	1b1h	A	149	506	2.8e-27	0.13	0.87		HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B; IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1042	1b1h	A	150	515	8.5e-45	0.37	0.80		HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B; IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1042	1b1h	A	46	417	3.4e-48			130.68	HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B; IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1042	1b1h	A	50	417	3.4e-48	0.15	1.00		HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B; IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION



Table 5

SEQ ID NO.	PDB ID	CHAIN N ID	STAR T AA	END AA	Pat Blast	Verify score	PMF score	SEQIDOL D score	Compound	PDB annotation
1042	1bn3	H	336	519	1.3e-50	0.14	0.09		IMMUNOGLOBULIN OP02 FAB, CONSTANT DOMAIN; CHAIN: L; IMMUNOGLOBULIN OP02 FAB, VARIABLE DOMAIN; CHAIN: H	IMMUNE SYSTEM IMMUNOGLOBULIN
1042	1c5c	H	336	519	2.8e-51	0.10	0.06		CHIMERIC DECARBOXYLASE ANTIBODY 21D8; CHAIN: L; CHIMERIC DECARBOXYLASE ANTIBODY 21D8; CHAIN: H	IMMUNE SYSTEM IMMUNOGLOBULIN, CATALYTIC ANTIBODY, CHIMERIC FAB, 2 DECARBOXYLASE, HAPTEN COMPLEX
1042	1c6c	B	336	515	5.6e-51	-0.00	-0.02		IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D	IMMUNOGLOBULIN, FAB COMPLEX, IDIOTYPE, ANTI-IDIOTYPE
1042	1c6c	B	48	244	2.8e-72	0.16	-0.06		IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D	IMMUNOGLOBULIN, FAB COMPLEX, IDIOTYPE, ANTI-IDIOTYPE
1042	1c17	I	434	519	7e-25	0.08	0.09		IGG1 ANTIBODY 1696 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 1696 (VARIABLE HEAVY CHAIN); CHAIN: H; IGG1 ANTIBODY 1696	IMMUNE SYSTEM IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1 FAB FRAGMENT, CROSS-REACTIVITY, HIV1 PROTEINASE, ENZYME 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verity score	PMF score	SEQPOL D score	Compound	PDB annotation
1042	1eqk	A	418	516	1.4e-25	0.23	-0.11		(CONSTANT HEAVY CHAIN, CHAIN: H; CH3 DOMAIN OF MAK3 ANTIBODY; CHAIN: A, B;	INHIBITION, IMMUNOGLOBULIN IMMUNE SYSTEM CONSTANT DOMAIN, C1-SUBSET, IMMUNOGLOBULIN, IMMUNE SYSTEM
1042	1es6	A	135	515	3.4e-46	0.31	0.62		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1042	1es6	A	149	517	1.4e-35	0.19	0.77		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1042	1es6	A	244	602	1.1e-34	0.11	0.46		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1042	1es6	A	43	418	1.7e-56			125.44	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1042	1es6	A	50	416	1.7e-56	-0.10	0.71		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1042	1dgt	R	131	416	5.1e-28	-0.23	0.47		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS VIRAL PROTEIN, RECEPTOR CD155, PYR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS VIRAL PROTEIN, RECEPTOR
1042	1dgt	R	49	331	3.4e-43			112.84	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS VIRAL PROTEIN, RECEPTOR CD155, PYR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS VIRAL PROTEIN, RECEPTOR
1042	1dgt	R	52	331	3.4e-43	-0.28	0.05		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS VIRAL PROTEIN, RECEPTOR CD155, PYR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS VIRAL PROTEIN, RECEPTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1042	1dh2	A	250	415	1.3e-35	-0.05	0.07		IMMUNOGLOBULIN LAMPDA HEAVY CHAIN; CHAIN: A; B; ENGINEERED PEPTIDE; CHAIN: E; F;	RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1042	1ek	A	244	415	1.4e-36	-0.26	0.06		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A; B;	COMPLEX CD16, IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
1042	1ek	H	336	518	4.2e-51	0.32	0.27		TAB2; CHAIN: L; M; TAB2; CHAIN: H; I; CYCLIC PEPTIDE; CHAIN: P; O	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN-PEPTIDE RECOGNITION
1042	1ek	H	48	247	1.4e-74	0.08	-0.11		TAB2; CHAIN: L; M; TAB2; CHAIN: H; I; CYCLIC PEPTIDE; CHAIN: P; O	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN-PEPTIDE RECOGNITION
1042	1ek	B	49	241	1.1e-65	-0.06	0.29		CATALYTIC ANTIBODY I788 COMPLEXED WITH PHENYL [1-(1-N-SUCCINYLAMINO)PENTYL] LEAP 3	
1042	1eg0	H	51	244	1.1e-65	0.05	0.00		PHOSPHONATE LEAP 4 IGG2A MONOCLONAL ANTIBODY (LIGHT CHAIN); CHAIN: L; IGG2A MONOCLONAL ANTIBODY (HEAVY CHAIN); CHAIN: H; PMDV PEPTIDE; CHAIN:	IMMUNE SYSTEM EMPLOY, ANTIGENIC-ANTIBODY INTERACTIONS, RGD MOTIF, G-H LOOP 2 OF VP1

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1042	1ert	C	247	416	8.5e-27	0.27	0.88		P <sub>1</sub> FIBROBLAST GROWTH FACTOR 1; CHAIN: A. B: FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D.	GROWTH FACTOR/GROWTH FACTOR 1; CHAIN: A. B: FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D.
1042	12q	A	250	420	1.2e-26	0.13	0.87		HIGH AFFINITY IMAMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A.	IMMUNE SYSTEM FC-EPSILON R-ALPHA; IMAMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1042	16a	A	246	420	5.1e-31	0.06	0.72		HIGH AFFINITY IMAMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IGE EPSILON CHAIN C REGION; CHAIN: B, D.	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMAMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1042	16i	H	48	241	8.4e-68	0.07	-0.05		IMAMUNOGLOBULIN FAB FRAGMENT FROM A MONOCLONAL ANTILIBSONATE ANTIBODY, R19.9 IPAL3 (IGG2B,KAPPA) IPAL4	
1042	16i	H	48	244	1.1e-72	0.05	-0.17		COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE MONOCLONAL ANTIBODY P9.13.7 (IGG1) IPH1.3 COMPLEXED WITH LY8027MB (E.C.3.2.1.17) IPH1.4	
1042	162	D	250	415	7e-36	0.07	0.06		IMAMUNOGLOBULIN FC	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1042	1f6n	H	337	514	7e-51	0.11	0.48		AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	IMMUNOGLOBULIN FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN, ANTIBODY, FAB, ANTI-TF, MONOCLONAL, MURINE, IMMUNOGLOBULIN
1042	1f65	H	54	244	8.4e-66	0.14	0.07		MONOCLONAL ANTIBODY MAK33; CHAIN: L; MONOCLONAL ANTIBODY MAK33; CHAIN: H;	IMMUNE SYSTEM FAB, BIP, CRYSTAL STRUCTURE
1042	1f63	A	51	243	7e-66	-0.02	0.06		BLUE FLUORESCENT ANTIBODY (19G2)-HEAVY CHAIN; CHAIN: H, A: BLUE FLUORESCENT ANTIBODY (19G2)-LIGHT CHAIN; CHAIN: L, B;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1042	1f6r	H	50	244	4.2e-72	0.03	-0.06		IMMUNOGLOBULIN 1GGA2 FAB FRAGMENT (FAB17.1A) (ORTHORHOMBIC CRYSTAL FORM) 1FOR 3	
1042	1f6k	C	336	519	1.4e-50	0.11	0.01		MAJOR POLLEN ALLERGEN BET V 1-A; CHAIN: A, D, G, F; IMMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, E, H, K; ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F;	IMMUNE SYSTEM BET V 1-A, BETV1 ALLERGEN; BV16 FAB-FRAGMENT, KAPPA MOEC21 CODING SEQUENCE, HEAVY CHAIN OF THE MONOCLONAL ANTIBODY NS12, BET V 1, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
1042	1tsk	C	48	244	2.8e-72	0.05	-0.14		I, L <sub>1</sub> MAJOR POLLEN ALLERGEN BET V I-A; CHAIN: A, D, G, J; IMMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, E, H, K <sub>2</sub> ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F, L <sub>1</sub>	IMMUNE SYSTEM BET V I-A, BET V ALLERGEN; BV16 FAB-FRAGMENT, KAPPA MOPC21 CODING SEQUENCE; HEAVY CHAIN OF THE MONOCLONAL ANTIBODY M872; BET V I, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX
1042	1bh6	B	50	246	1.1e-70	0.29	0.22		IGG2A KAPPA ANTIBODY CB41 (LIGHT CHAIN); CHAIN: A; IGG2A KAPPA ANTIBODY CB41 (HEAVY CHAIN); CHAIN: B; PEPTIDE 5; CHAIN: C <sub>1</sub>	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1
1042	1hzh	H	163	521	4.2e-63	0.12	0.55		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K <sub>1</sub> IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L <sub>1</sub> , M <sub>1</sub>	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12
1042	1hzh	H	48	418	0	0.28	0.55		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K <sub>1</sub> IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L <sub>1</sub> , M <sub>1</sub>	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12
1042	1hzh	H	4	320	1.4e-51	-0.22	0.81		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K <sub>1</sub> IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L <sub>1</sub> , M <sub>1</sub>	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pat Blast	Verity score	PMF score	SEQ/ROL D score	Compound	PDB annotation
1042	1ile	A	251	415	7e-50	0.07	-0.11		IG GAMMA-2A CHAIN C REGION; CHAIN: A, B	IMMUNE SYSTEM IGG2A, IGG, FC
1042	1ibg	H	49	241	5.6e-67	0.10	0.13		IMMUNOGLOBULIN IGG FAB (IGG2B, KAPPA) FRAGMENT (40-50 FAB) COMPLEXED WITH IIBG 3 OLUBAIN IIBG 4	
1042	1igt	B	160	517	9.8e-61	-0.03	0.54		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT REGION, IMMUNOGLOBULIN
1042	1igt	B	49	415	0	0.10	0.66		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT REGION, IMMUNOGLOBULIN
1042	1igt	B	51	475	0			102.57	IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT REGION, IMMUNOGLOBULIN
1042	1igt	B	5	318	2.8e-48	-0.12	0.28		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT REGION, IMMUNOGLOBULIN
1042	1igy	B	160	516	5.6e-61	0.04	0.64		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT REGION, IMMUNOGLOBULIN
1042	1igy	B	49	415	0	-0.03	0.31		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT REGION, IMMUNOGLOBULIN
1042	1ili	A	50	244	7e-68	0.06	-0.02		MONOCLONAL ANTIBODY G3-519 (HEAVY CHAIN); CHAIN: A; MONOCLONAL ANTIBODY G3-519 (LIGHT CHAIN); CHAIN: B;	IMMUNE SYSTEM FAB, BETA SHEET STRUCTURE, ANTIBODY
1042	1ilb	B	261	517	1e-36	0.15	0.71		INTERLEUKIN-1 BETA; CHAIN: A, TYPE 1	COMPLEX (IMMUNOGLOBULIN/RECEPTOR)

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	P4 Blast	Verity score	PMF score	SEQ/FOLD score	Compound	PDB annotation
1042	1kbs	H	49	244	2.3e-72	0.10	0.06		INTERLEUKIN-1 RECEPTOR, CHAIN: B <sub>3</sub>	IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1042									KB3-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H <sub>2</sub>	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) FOR VAPLEHA V BETA DOMAIN- T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
1042	Imco	H	189	516	1.1e-67	0.05	0.01		IMMUNOGLOBULIN (IGG1) (MCG) WITH A HINGE DELETION IMCO	
1042	Imco	H	48	415	0	0.05	0.66		IMMUNOGLOBULIN (IGG1) (MCG) WITH A HINGE DELETION IMCO	
1042	Imco	H	49	475	0			106.26	IMMUNOGLOBULIN (IGG1) (MCG) WITH A HINGE DELETION IMCO	
1042	Imco	H	5	320	2.8e-55	-0.30	0.09	3	IMMUNOGLOBULIN (IGG1) (MCG) WITH A HINGE DELETION IMCO	
1042	Imcp	H	49	231	1.1e-48	-0.07	0.11	3	IMMUNOGLOBULIN (IGG1) (MCG) WITH A HINGE DELETION IMCO	



Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL ID score	Compound	PDB annotation
1042	1mbb	B	336	519	1.4e-50	0.16	0.07		1MCP 4 IMMUNOGLOBULIN FAB D44.1 (GG1,KAPP A) (BALB/C MOUSE, MONOCLONAL ANTIBODY) 1M.B.5	
1042	1p6c		417	520	2.8e-23	0.02	-0.13		IMMUNOGLOBULIN SP75C(PRIABD) FRAGMENT OF AN IGG1 IPRC 4	
1042	1p6g	H	48	243	4.2e-73	0.17	-0.05		IGG2A-KAPP A-1 IPRG 4 CHAIN: L, H, IPRG 5	IMMUNOGLOBULIN
1042	1p6k	H	49	240	1.4e-61	-0.17	0.04		ANTIBODY: CHAIN: L, H	IMMUNOGLOBULIN FAB, GD2-GANGLIOSIDE, CARBOHYDRATE, MELANOMA, IMMUNOGLOBULIN
1042	1qfu	H	336	518	1.3e-50	0.30	0.28		HEMAGGLUTININ (HA1 CHAIN): CHAIN: A; HEMAGGLUTININ (HA2 CHAIN): CHAIN: B; IMMUNOGLOBULIN IGG1-KAPP A ANTIBODY (LIGHT CHAIN): CHAIN: L; IMMUNOGLOBULIN IGG1-KAPP A ANTIBODY (HEAVY CHAIN): CHAIN: H;	VIRAL PROTEIN/IMMUNE SYSTEM COMPLEX (HEMAGGLUTININ/IMMUNOGLOBULIN, HEMAGGLUTININ, 2 IMMUNOGLOBULIN, VIRAL PROTEIN/IMMUNE SYSTEM
1042	1qfu	H	48	244	1.4e-72	0.10	-0.11		HEMAGGLUTININ (HA1 CHAIN): CHAIN: A; HEMAGGLUTININ (HA2 CHAIN): CHAIN: B; IMMUNOGLOBULIN IGG1-KAPP A ANTIBODY (LIGHT CHAIN): CHAIN: L; IMMUNOGLOBULIN IGG1-KAPP A ANTIBODY	VIRAL PROTEIN/IMMUNE SYSTEM COMPLEX (HEMAGGLUTININ/IMMUNOGLOBULIN, HEMAGGLUTININ, 2 IMMUNOGLOBULIN, VIRAL PROTEIN/IMMUNE SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1042	1wee	H	51	244	1.4e-66	-0.10	0.18		(HEAVY CHAIN); CHAIN: H; TR19 FAB; CHAIN: L; H;	IMMUNOGLOBULIN TR19, ANTI-THYROID PEROXIDASE, AUTOANTIBODY, 2 IMMUNOGLOBULIN
1042	1wej	H	336	520	8.4e-51	0.24	0.27		E8 ANTIBODY; CHAIN: L; H; CYTOCHROME C <sub>2</sub> CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C <sub>2</sub> ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C <sub>2</sub> COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
1042	1wej	H	50	244	8.4e-69	0.18	-0.01		IG ANTIBODY D2.3 (LIGHT CHAIN); CHAIN: L; IG ANTIBODY D2.3 (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM ABZVME-TRANSITION STATE ANALOG, IMMUNE SYSTEM
1042	25e8	H	336	515	1.4e-51	0.11	0.16		IGG 508; CHAIN: L; H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
1042	2bfj	H	49	231	7e-51	-0.03	0.04		IMMUNOGLOBULIN IGP-A FAB FRAGMENT (4539) (GALACTAN-BINDING) 2FBL3	
1042	26eb	A	249	419	3.4e-28	0.11	0.74		PG GAMMA RIB; CHAIN: A;	IMMUNE SYSTEM CD32-RECEPTOR, PG, CD32, IMMUNE SYSTEM
1042	36ct	B	336	518	4.2e-50	0.22	0.09		METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A; C; METAL CHELATASE	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT, IMMUNE 2 SYSTEM

Table 5

SEQ ID NO.	PDB ID	CHAI N ID	STAR TAA	END AA	PI Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
									CATALYTIC ANTIBODY; CHAIN: B, D	
1043	1cdq		88	164	8.4e-20	0.59	1.00		COMPLEMENT REGULATORY PROTEIN CD59 (NMR, 20 STRUCTURES) 1CDQ 3	
1043	1cdq		88	164	8.4e-20			142.11	COMPLEMENT REGULATORY PROTEIN CD59 (NMR, 20 STRUCTURES) 1CDQ 3	
1043	1erg		88	157	2.8e-19	0.41	1.00		COMPLEMENT FACTOR HUMAN COMPLEMENT REGULATORY PROTEIN CD59 (EXTRACELLULAR 1ERG 3 REGION, RESIDUES 1 - 70) (NMR, RESTRAINED MINIMIZED 1ERG 4 AVERAGE STRUCTURE) 1ERG 5	
1043	1erg		88	157	2.8e-19			131.94	COMPLEMENT FACTOR HUMAN COMPLEMENT REGULATORY PROTEIN CD59 (EXTRACELLULAR 1ERG 3 REGION, RESIDUES 1 - 70) (NMR, RESTRAINED MINIMIZED 1ERG 4 AVERAGE STRUCTURE) 1ERG 5	
1047	1aln	A	11	199	0			232.06	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHCI, HLA-B*3501, HIV, 2 NER, COMPLEX

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/FOI D score	Compound	PDB annotation
1047	1aln	A	25	299	0			410.38	B*3501: CHAIN: A, B; PEPTIDE: VPLRMATY; CHAIN: C;	(ANTIGEN/PEPTIDE) COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1047	1aln	A	25	300	0	0.83	1.00		B*3501: CHAIN: A, B; PEPTIDE: VPLRMATY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1047	1agd	A	11	199	0			233.86	B*0801: CHAIN: A, BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKRYKL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1047	1agd	A	25	299	0			411.64	B*0801: CHAIN: A, BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKRYKL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1047	1agd	A	25	300	0	0.79	1.00		B*0801: CHAIN: A, BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKRYKL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1047	1elx	A	25	302	0	0.87	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1047	1efx	A	25	302	0			420.37	CHAIN: B: PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C: NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D: E: HLA-CW3 (HEAVY CHAIN); CHAIN: A: BETA-2-MICROGLOBULIN; CHAIN: B: PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C: NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D: E: CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX	
1047	1hsa	A	11	199	0			232.10	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HSA 3 /HLA-B*ASTERSKJ27055 HSA 4	
1047	1hsa	A	25	299	0			410.78	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HSA 3 /HLA-B*ASTERSKJ27055 HSA 4	
1047	1hsa	A	25	300	0	0.82	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HSA 3 /HLA-	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQPOL ID score	Compound	PDB annotation
1047	1hsb	A	11	199	0			257.74	BACTERIOPHAGE T7055 HISA 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE HSB 3 ANTIGEN) HSB 4
1047	1hsb	A	25	294	0	0.86	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE HSB 3 ANTIGEN) HSB 4	IMMUNE SYSTEM MAJOR ANTIGEN, MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUCOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1047	1hsb	A	25	294	0			414.03	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE HSB 3 ANTIGEN) HSB 4	
1047	1hsb	A	11	199	1.4e-100			265.59	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN, A, BETA-2-MICROGLOBULIN, CHAIN, B, MELANOMA-ASSOCIATED ANTIGEN 4, CHAIN, C	IMMUNE SYSTEM MAJOR ANTIGEN, MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUCOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1047	1hsb	A	25	299	0	0.83	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN, A, BETA-2-MICROGLOBULIN, CHAIN, B, MELANOMA-ASSOCIATED ANTIGEN	IMMUNE SYSTEM MAJOR ANTIGEN, MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUCOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/POI D score	Compound	PDB annotation
1047	1q4f	A	25	299	0			435.50	4; CHAIN: C; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1047	1q4d	A	12	199	0			232.33	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-C*W4 CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HLA-C*W4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1047	1q4d	A	26	298	0	0.87	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-C*W4 CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HLA-C*W4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1047	1q4d	A	26	298	0			407.96	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-C*W4 CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HLA-C*W4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1047	1q4d	A						284.63	HISTOCOMPATIBILITY ANTIGEN TRUNCATED	

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Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQ/TOOL D score	Compound	PDB annotation
1048	1efk	A	11	199	0			241.21	HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*01:01 (IMC3 COMPLEXED WITH A DECAMERIC PEPTIDE (GVAAPEYHRK) IMC 4	IMMUNE SYSTEM MHC, HLA CLASS I, KIR, NK CELL RECEPTOR, INAMNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1048	2ebo	A	12	88	4.2e-18	-0.74	0.29		EBOLA VIRUS ENVELOPE GLYCOPROTEIN; CHAIN: A, B, C, G	ENVELOPE GLYCOPROTEIN ENVELOPE GLYCOPROTEIN, FILOVIRUS, EBOLA VIRUS, GP2, COAT 2 PROTEIN
1050	1edy		32	133	3.4e-07	0.40	0.19		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN INAMNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1050	1ldj	R	25	127	2.8e-29	0.41	0.46		POLIOVIRUS RECEPTOR; CHAIN: R, VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/INTRAL PROTEIN RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1050	1d9	A	32	126	8.5e-10	0.33	0.06		T LYMPHOCYTE ACTIVATION ANTIGEN; CHAIN: A;	IMMUNE SYSTEM B7-1 (CD80), IG SUPERFAMILY
1050	1eaj	A	33	127	1.7e-07	0.41	-0.03		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUSVIRAL PROTEIN RECEPTOR COXSACKIEVIRUS B-ADENOVIRUS RECEPTOR, HCAR, VIRUSVIRAL PROTEIN RECEPTOR, IMMUNOGLOBULIN V DOMAIN FOLD, 2 SYMMETRIC DIMER
1050	1bwm	B	20	123	1.5e-06	0.36	0.06		GAMMA-DELTA T-CELL RECEPTOR; CHAIN: A, C, E, G; GAMMA-DELTA T-CELL RECEPTOR; CHAIN: B, D, F, H;	IMMUNE SYSTEM T-CELL RECEPTOR DELTA CHAIN; T-CELL RECEPTOR GAMMA CHAIN; IG DOMAIN, T CELL RECEPTOR, TCR, GPCR
1050	1i8l	C	33	120	8.5e-06	0.12	0.80		T LYMPHOCYTE ACTIVATION ANTIGEN CD88; CHAIN: A, B;	IMMUNE SYSTEM ACTIVATION RECEPTOR CTLA-4 COINTEGRATOR, T-LYMPHOCYTE-ASSOCIATED ANTIGEN RECEPTORS, INHIBITORY COMPLEX
1050	1i1l	G	32	131	7e-06	0.21	-0.03		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/RECEPTOR FGFR-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREPOIL
1050	1neu		27	128	6.8e-11	0.56	0.13		MYELIN P0 PROTEIN; CHAIN: NULL;	STRUCTURAL PROTEIN MYELIN, GLYCOPROTEIN, TRANSMEMBRANE, PHOSPHORYLATION, IMMUNOGLOBULIN FOLD, SIGNAL, MYELIN 2 MEMBRANE

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Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1050	2c60	A	29	127	8.4e-06	0.35	0.31		BENC-JONES PROTEIN W/ A VARIABLE DOMAIN FROM CHAIN: A, B;	ADHESION MOLECULE IMMUNE SYSTEM IMMUNOGLOBULIN, BENC-JONES PROTEIN, LAMBDA-6
1052	1tgx	A	55	98	0.0031	-0.49	0.01		CTOTOXIN TOXIN GAMMA (CARDIOTOXIN) ITGX 3	
1052	2czt		55	98	0.0023	-0.25	0.00		CARDIOTOXIN CARDIOTOXIN III (NMR, 13 STRUCTURES) 2CZS 3	
1054	1a3e		117	272	8.4e-20			74.90	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1054	1awc	B	95	244	7e-38			75.28	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA, GABP BETA; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1054	1bd8		93	247	4.2e-31			71.99	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1054	1btk	B	95	250	2.8e-31			71.23	CYC LIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR, PROTEIN, CYC LIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1054	1bw9	A	91	255	4.2e-33			80.55	CYC LIN-DEPENDENT	HORMONE/GROWTH FACTOR

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMR score	SEQPOL ID score	Compound	PDB annotation
									KINASE 6 INHIBITOR, CHAIN: A;	P18-INK4C, CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE
1054	1by2		1	113	8.4e-44			114.47	MAC-2 BINDING PROTEIN; CHAIN: NULL;	HORMONE-GROWTH FACTOR EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K, EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1054	1by2		711	824	7e-44			113.40	MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K, EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1054	1by2		714	822	7e-44	0.79	1.00		MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K, EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1054	1ctu	A	217	709	1.4e-74			146.51	SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE BETA-PROPELLER, SUPRABARREL, COMPLEX WITH THE COPACTOR P002 AND THE INHIBITOR METHYLHYDRAZINE, OXIDOREDUCTASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast score	Verify score	PMF score	SEQ/PROL ID score	Compound	PDB annotation
1054	1etu	A	218	645	1.4e-74	0.34	0.92		SOLUBLE QUINOROTEN GLUCOSE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE BETA- PROPELLER, SUPERBAREL, COMPLEX WITH THE COFACTOR POQ 2 AND THE INHIBITOR METHYLHYDRAZINE, OXIDOREDUCTASE
1054	1d9s	A	2	129	2.8e-07			51.72	CYCLOIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX- TURN-HELIX, ANKYRIN REPEAT
1054	1hhb	A	96	246	4.2e-53			78.44	CYCLOIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- INK4(INK6); CELL CYCLE INHIBITOR, P18-INK4(INK6), ANKYRIN REPEAT 2 CDK 4/6 INHIBITOR
1054	1jln	D	95	296	2.8e-38			80.27	NF-KAPPA-B P65 SUBUNIT; CHAIN: A, NF- KAPPA-B P50D SUBUNIT; CHAIN: C, I- KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D- TRANSCRIPTION FACTOR, IKB/NFkB COMPLEX
1054	1myo		127	244	1.3e-26			72.80	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK- REPEAT
1054	1nfi	E	87	292	5.6e-38			75.42	NF-KAPPA-B P65; CHAIN: A, C, NF-KAPPA- B P50; CHAIN: B, D, I- KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGAN REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1057	1e9t	A	220	269	1.3e-11	0.15	-1202.08		INTESTINAL TREFOIL FACTOR; CHAIN: A;	CELL MOTILITY FACTOR HIF, INTESTINAL TREFOIL FACTOR, SOLUTION STRUCTURE, TREFOIL, 2 DOMAIN, NMR SPECTROSCOPY, CELL MOTILITY FACTOR
1057	1ht7	A	222	275	7.5e-16	0.26	-1202.08		P52 PROTEIN; CHAIN: A;	GROWTH FACTOR FNR-

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEOTOL D score	Compound	PDB annotation
									B;	2 P52 T81 BREAST CANCER HISTOGEN INDUCIBLE GROWTH FACTOR, CELL MOTILITY, TUMOR SUPPRESSOR, TREHOIL 2 DOMAIN, SIGNAL
1057	2psp	A	223	269	1.5e-11	0.35	-1202.08		PORCINE PANCREATIC SPASMOLYTIC POLYPEPTIDE; CHAIN: A, B;	TREHOIL FAMILY OF PEPTIDES P5P REPEAT, GROWTH FACTOR, SIGNAL
1063	1aln	A	29	255	0	0.27	-1202.08		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35: MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA-B*3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1063	1a6z	A	22	227	1.1e-68			53.05	HFE, CHAIN: A, C, BETA-2-MICROGLOBULIN; CHAIN: B, D	MHC CLASS I COMPLEX HFE, HEREDITARY HEMOCHROMATOSIS, MHC CLASS I
1063	1a6z	A	29	255	1.4e-68			59.25	HFE, CHAIN: A, C, BETA-2-MICROGLOBULIN; CHAIN: B, D	MHC CLASS I COMPLEX HFE, HEREDITARY HEMOCHROMATOSIS, MHC CLASS I
1063	1a6d	A	29	255	0	0.36	-1202.08		B*0801; CHAIN: A, BETA-2-MICROGLOBULIN; CHAIN: B, HIV-1 GAG PEPTIDE (GGKKKCYTL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8: B2M; PEPTIDE HLA-B8, HIV, MHC CLASS I HISTOCOMPATIBILITY COMPLEX
1063	1c16	A	29	255	2.8e-67			50.68	MHC-LIKE PROTEIN T22; CHAIN: A, C, B, G, BETA-2-MICROGLOBULIN; CHAIN: B, D, F, H	IMMUNE SYSTEM NON-CLASSICAL MHC-LIKE, MAJOR HISTOCOMPATIBILITY, BETA2-2 MICROGLOBULIN
1063	1d2v	C	118	585	0			522.22	MYELOPEROXIDASE;	OXIDOREDUCTASE HEME-

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Table 5

SFQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Bias	Verify score	PAP score	SRCOOL D score	Compound	PDB annotation
									CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D	PROTEIN PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE-2-BROMIDE COMPLEX
1063	1ed3	A	29	255	0	0.40	-1202.08		CLASS I MAJOR HISTOCOMPATIBILITY ANTIGEN RT1-AA; CHAIN: A, D; BETA-2-MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTF-E (I3N3B); CHAIN: C, F;	IMMUNE SYSTEM MAJOR HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 HISTOCOMPATIBILITY COMPLEX, MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1063	1ed3	A	29	255	0			58.49	CLASS I MAJOR HISTOCOMPATIBILITY ANTIGEN RT1-AA; CHAIN: A, D; BETA-2-MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTF-E (I3N3B); CHAIN: C, F;	HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 HISTOCOMPATIBILITY COMPLEX, MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1063	1ed3	A	29	255	0	0.44	-1202.08		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1063	1ed3	A	29	255	0			57.25	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fa Blast	Verify score	PMF score	SEFOL D score	Compound	PDB annotation
									MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D; E;	FOLD, RECEPTOR/MHC COMPLEX
1063	1l2k	A	29	255	5.6e-98			58.77	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN; A; BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID PROTEIN; CHAIN: P;	IMMUNE SYSTEM SEV9, MAJOR HISTOCOMPATIBILITY PEPTIDE-MHC
1063	1hoc	A	29	255	2.8e-98			50.16	HISTOCOMPATIBILITY ANTIGEN NIURNE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D-B*5, B2-MICROGLOBULIN, AND A 9*RESIDUE PEPTIDE 1HOC 4	
1063	1hsa	A	29	255	0	0.24	-1202.08		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B*45TERUSKJ27055 1HSA 4	
1063	1hsb	A	29	255	0	0.40	-1202.08		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AV68.1	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Bias	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1063	1hnb	A	29	255	0			52.66	(LEUCOCYTE HSB 3 ANTIGEN) HSB 4	
									HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE HSB 3 ANTIGEN) HSB 4	
1063	1hyr	C	21	227	8.4e-55			52.26	NIK2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B; A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C	IMMUNE SYSTEM NEK2D; MIC-A, MIC, PERB1; ACTIVATING NK CELL RECEPTOR, NK2D, C-TYPE-LECTIN LIKE, MIC-2 A, MHC-1 COMPLEX, IMMUNE SYSTEM
1063	1hyr	C	28	255	1.4e-53			67.13	NIK2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B; A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C	IMMUNE SYSTEM NEK2D; MIC-A, MIC, PERB1; ACTIVATING NK CELL RECEPTOR, NK2D, C-TYPE-LECTIN LIKE, MIC-2 A, MHC-1 COMPLEX, IMMUNE SYSTEM
1063	14f	A	29	255	0	0.47	-1202.08		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1063	14f	A	29	255	0			60.36	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN



Table 5

Seq ID No:	PDB ID	CHAIN ID	STAR T	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1063	1ld9	A	29	254	0			56.90	4; CHAIN: C; MHC CLASS I H-2D HEAVY CHAIN: CHAIN: A: BETA-2 MICROGLOBULIN; CHAIN: B: NANO- PEPTIDE; CHAIN: C;	MAJOR HISTOCOMPATIBILITY COMPLEX I.D. MAJOR HISTOCOMPATIBILITY COMPLEX, LD
1063	1ld9	A	29	255	0	0.20	-1202.08		MHC CLASS I H-2D HEAVY CHAIN: CHAIN: A: BETA-2 MICROGLOBULIN; CHAIN: B: NANO- PEPTIDE; CHAIN: C;	MAJOR HISTOCOMPATIBILITY COMPLEX I.D. MAJOR HISTOCOMPATIBILITY COMPLEX, LD
1063	1qo3	A	30	255	0	0.46	-1202.08		MHC CLASS I H-2D HEAVY CHAIN: CHAIN: A: BETA-2 MICROGLOBULIN; CHAIN: B: HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C; D;	COMPLEX ONE RECEPTOR/MHC CLASS I H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M, NK-CELL SURFACE GLYCOPROTEIN YEA48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-1TYPE 1 FECTIN-LIKE 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1063	1qo3	A	30	255	0			54.24	MHC CLASS I H-2D HEAVY CHAIN: CHAIN: A: BETA-2 MICROGLOBULIN; CHAIN: B: HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C; D;	COMPLEX ONE RECEPTOR/MHC CLASS I H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M, NK-CELL SURFACE GLYCOPROTEIN YEA48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-1TYPE 1 FECTIN-LIKE 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1063	1qo4	A	30	255	0	0.20	-1202.08		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-C/MW CHAIN: A; BETA-2	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	
1063	1qgd	A	30	255	0			53.86	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-C*W4 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (G)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1063	1tmc	A	22	192	9.8e-79			68.60	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 1TMC3 COMPLEXED WITH A DECAAMERIC PEPTIDE (EVAPPEYHRK) 1TMC4	
1063	1zng	A	29	255	5.6e-62			55.36	ZINC-ALPHA-2-GLYCOPROTEIN; CHAIN: A, B, C, D;	LIPID MOBILIZATION FACTOR ZN-ALPHA-2-GLYCOPROTEIN, ZAG LIPID MOBILIZATION FACTOR, SECRETED MHC CLASS I HOMOLOG
1065	1aej	A	71	336	4.2e-29	0.11	-1202.08		PHOSPHOGLYCERATE MUTASE; CHAIN: A;	ISOMERASE ALPHA/BETA-TYPE STRUCTURE
1065	12e8	H	2	227	8.4e-09			59.62	2E8 (GGG-KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
1065	1bth	A	29	376	1.1e-29			78.69	HEMOGLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1066	1b1h	A	30	346	1.1e-29	0.07	-1202.08		HEMOLIN; CHAIN: A, B.	INSECT IMMUNITY INSECT IMMUNITY, IPS BINDING, HOMOPHILIC ADHESION
1066	1a6f	A	20	376	2.8e-35			85.17	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1066	1cvs	D	122	302	7e-31	0.12	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FOR FGF, FGF, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1066	1cvs	D	37	208	2.8e-23	0.25	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FOR FGF, FGF, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1066	1dgi	R	12	303	9e-22			63.55	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1066	1e12	G	132	308	4.2e-30	0.09	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FOR FGF, FGF, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1066	1e12	C	37	208	2.8e-22	0.16	-1202.08		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FOR FGF, FGF, IMMUNOGLOBULIN-LIKE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.A.A	END AA	Pdb blast	Verity score	PMF score	SICOPOL D score	Compound	PDB annotation
									FACTOR RECEPTOR I; CHAIN: C, D <sub>3</sub>	DOMAINS BELONGING TO THE I-SIT 2 SUBGROUP WITHIN IG-LIKE DOMAINS. R-TRTFOI. FOLD
1066	1f2q	A	121	308	8.4e-23	0.18	-1202.08		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A <sub>1</sub>	IMMUNE SYSTEM FC-EPSILON R-ALPHA IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1066	1f2q	A	26	214	4.2e-28			66.45	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A <sub>1</sub>	IMMUNE SYSTEM FC-EPSILON R-ALPHA IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1066	1f2q	A	28	214	4.2e-28	0.23	-1202.08		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A <sub>1</sub>	IMMUNE SYSTEM FC-EPSILON R-ALPHA IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1066	1f42	A	21	325	1.2e-08			63.76	INTERLEUKIN-12 BETA CHAIN, CHAIN: A <sub>1</sub>	CYTOKINE CYTOKINE
1066	1f6a	A	24	213	1.4e-29			75.69	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A <sub>1</sub> IG EPSILON CHAIN C REGION; CHAIN: B, D <sub>2</sub>	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1066	1f6a	A	24	214	1.4e-29	0.42	-1202.08		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A <sub>1</sub> IG EPSILON CHAIN C REGION; CHAIN: B, D <sub>2</sub>	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1066	1f8r	H	2	227	4.2e-08			66.69	ANTIBODY FAB FRAGMENT (LIGHT	IMMUNE SYSTEM MONOCLONAL ANTIBODY, ANTIGEN-BINDING

Table 5

SEQ ID	PDB ID	CHAIN ID	STAR T.AA	END AA	Pat Bias	Verify score	PMF score	SEOROL D score	Compound	PDB annotation
									CHAIN: CHAIN: L; ANTIBODY FAB FRAGMENT (HEAVY CHAIN: CHAIN: H MOLECULE; CHAIN: A;	FRAGMENT, INTERLEUKIN-2, X-RAY ANALYSIS, CRYSTAL
1066	1f97	A	101	309	14e-29			72.64	JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1066	1f6g	A	120	305	3e-23	0.14	-1202.08		FC RECEPTOR; FC(GAMMA)RLA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR; IMMUNOGLOBULIN, LEUKOCYTE, CD32
1066	1f6g	A	23	210	84e-28			78.62	FC RECEPTOR; FC(GAMMA)RLA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR; IMMUNOGLOBULIN, LEUKOCYTE, CD32
1066	1f6l	A	117	307	1.5e-23	0.05	-1202.08		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1066	1f6l	A	22	211	7e-27			73.09	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1066	1f6l	A	28	212	7e-27	0.17	-1202.08		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1066	1g0x	A	118	310	2.8e-22			72.43	LEUCOCYTE IMMUNOGLOBULIN- LIKE RECEPTOR-1; CHAIN: A;	IMMUNE SYSTEM LEUKOCYTE INHIBITORY RECEPTOR-1; LEUKOCYTE IMMUNOGLOBULIN FOLD, 3-10 HELIX
1066	1g0x	A	120	297	9e-22	0.18	-1202.08		LEUCOCYTE IMMUNOGLOBULIN- INHIBITORY RECEPTOR-1;	IMMUNE SYSTEM LEUKOCYTE INHIBITORY RECEPTOR-1;

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T.A.	END A.A.	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1066	1g0x	A	120	306	2.8e-22	0.21	-1202.08		LIKE RECEPTOR-1; CHAIN: A;	LEUCOCYTE IMMUNOGLOBULIN FOLD, 3-10 HELIX
1066	1g0x	A	28	210	5.6e-26	0.21	-1202.08		LEUCOCYTE IMMUNOGLOBULIN- LIKE RECEPTOR-1; CHAIN: A;	IMMUNE SYSTEM LEUCOCYTE INHIBITORY RECEPTOR-1; LEUCOCYTE IMMUNOGLOBULIN FOLD, 3-10 HELIX
1066	1lgy	B	3	376	8.4e-09			65.38	IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1066	1lmo	H	2	376	5.6e-10			74.55	IMMUNOGLOBULIN G1 (GG1) (MCG) WITH A HINGE DELETION IMCO 3	
1066	1lnt		29	211	9.8e-26	0.21	-1202.08		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1066	1lnt		31	211	5.6e-33			71.40	P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1066	2dlf	A	119	304	2.8e-32	0.16	-1202.08		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR, KIR, NATURAL KILLER RECEPTOR, 2

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pa Blast	Verify score	PMF score	SEQUEST D score	Compound	PDB annotation
1066	2dli	A	216	331	9.8e-09	0.06	-1202.08		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNOGLOBULIN
1066	2dli	A	29	210	1.1e-24	0.43	-1202.08		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1066	2dli	A	31	213	2.8e-32			74.62	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1066	2dli	A	120	306	3e-23	0.14	-1202.08		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1066	2dli	A	23	214	1.4e-29			81.15	FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32 IMMUNE SYSTEM
1066	2dli	A	24	213	1.4e-29	0.12	-1202.08		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32 IMMUNE SYSTEM
1066	2dli	A	1	141	5.6e-33			52.09	NUMB PROTEIN; CHAIN: A; GPP1 PEPTIDE; CHAIN: B;	CELL CYCLE/GENE REGULATION TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTD), ASYMETRIC IC CELL DIVISION
1066	32c2	B	2	225	9.8e-09			60.00	IGG1 ANTIBODY 32C2; CHAIN: A; IGG1 ANTIBODY 32C2;	IMMUNE SYSTEM FAB; ANTIBODY, AROMATASE, P450

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1067	1hc2	A	8	64	2.8e-16			54.02	CHAIN: B; B3T1; CHAIN: A;	HYDROLASE INHIBITOR BOHIBINA S1EN TRYPTIN INHIBITOR BETA-SHEET DISULFIDE-RICH
1069	1hc6	B	1	299	0			340.18	FK506-BINDING PROTEIN; CHAIN: A, C; E, G; TOP-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1069	1hc6	B	253	586	0			351.53	FK506-BINDING PROTEIN; CHAIN: A, C; E, G; TOP-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1069	1hc6	B	264	581	0	0.64	-1202.08		FK506-BINDING PROTEIN; CHAIN: A, C; E, G; TOP-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1069	1es7	B	33	108	1.4e-12	0.14	-1202.08		BONE MORPHOGENETIC PROTEIN-2; CHAIN: A, C; BONE MORPHOGENETIC PROTEIN RECEPTOR I4; CHAIN: B, D;	CYTOKINE BMP-2; ALK-3; PROTEIN-PROTEIN COMPLEX, THREE FINGER TOXIN POLY, RECEPTOR-2 LIGAND COMPLEX, CYTOKINE RECEPTOR, TGF BETA SUPERFAMILY
1071	1aln	A	24	299	0			166.47	B*3501; CHAIN: A, B; PEPTIDE VP1RPMVY, CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN,



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1071	1aln	A	26	298	0	0.49	-1202.08		B*3501; CHAIN: A; B: PEPTIDE YPLRPMITY; CHAIN: C;	MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1071	1agd	A	24	299	0			169.42	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKCYKL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX (ANTIGEN/PEPTIDE)
1071	1agd	A	26	298	0	0.41	-1202.08		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKCYKL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1071	1e16	A	24	299	5.6e-69			139.27	MHC-LIKE PROTEIN T22; CHAIN: A, C, E, G; BETA-2-MICROGLOBULIN; CHAIN: B, D, F, H	IMMUNE SYSTEM NON-CLASSICAL MHC-LIKE, MAJOR HISTOCOMPATIBILITY, BETA2-2 MICROGLOBULIN
1071	1e43	A	24	300	0			157.88	CLASS I MAJOR HISTOCOMPATIBILITY ANTIGEN RT1-AA; CHAIN: A, D; BETA-2-MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTF-B (13NB); CHAIN: C, F;	IMMUNE SYSTEM MAJOR HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1071	1e43	A	26	298	0	0.52	-1202.08		CLASS I MAJOR	IMMUNE SYSTEM MAJOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ ID score	Compound	PDB annotation
1071	1etx	A	24	300	0			165.46	HISTOCOMPATIBILITY ANTIGEN RT1-A; CHAIN: A, D, BETA-2-MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTPE-13N3D; CHAIN: C, F;	HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 HISTOCOMPATIBILITY COMPLEX, MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1071	1etx	A	24	300	0			165.46	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1071	1etx	A	26	298	0	0.64	-1202.08		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1071	1etx	A	24	296	0			167.88	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN; A: BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID	IMMUNE SYSTEM SEV9, MAJOR HISTOCOMPATIBILITY COMPLEX PEPTIDE-MHC

Table 5

SEQ ID No:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Bias	Verify score	PMF score	SEQ/OL ID score	Compound	PDB annotation
1071	Ihoc	A	24	295	0			172.82	PROTEIN-CHAIN-P; HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING IHOC 3 OF H-2D-B*, P2-MICROGLOBULIN, AND A 2-RESIDUE PEPTIDE IHOC 4	
1071	Ihsa	A	24	299	0			167.79	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN ILSA 3 /HLA- B*ASTERSK2705S ILSA 4	
1071	Ihsa	A	26	298	0	0.49	-1202.08		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN ILSA 3 /HLA- B*ASTERSK2705S ILSA 4	
1071	Ihsb	A	24	293	0			166.59	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1071	Ihsb	A	26	293	0	0.46	-1202.08		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 3	

Table 5

SEQ ID NO.	PDB ID	CHAIN N ID	STAR T AA	END AA	Pat Blast	Verify score	PMF score	SPOFOL D score	Compound	PDB annotation
1071	1byr	C	10	193	2.8e-53			236.94	ANTIGEN0 HSB-4 NKG2D TYPE II INTERCAL MEMBRANE PROTEIN; CHAIN: B; A; MHC CLASS I CHAIN- RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D; MIC-A, MIC, PERB11; ACTIVATING NK CELL RECEPTOR, NKG2D, C- TYPE LECTIN LIKE, MIC-2 A, MIC-4, COMPLEX, IMMUNE SYSTEM
1071	1byr	C	23	297	6e-93			439.85	NKG2D TYPE II INTERCAL MEMBRANE PROTEIN; CHAIN: B; A; MHC CLASS I CHAIN- RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D; MIC-A, MIC, PERB11; ACTIVATING NK CELL RECEPTOR, NKG2D, C- TYPE LECTIN LIKE, MIC-2 A, MIC-4, COMPLEX, IMMUNE SYSTEM
1071	1h4f	A	24	298	0			168.36	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; MELANOMA- ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAJOR ANTIGEN, MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1071	1h4f	A	26	298	0	0.49	-1202.08		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; MELANOMA- ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAJOR ANTIGEN, MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1071	1h49	A	24	291	0			166.41	MHC CLASS I H-2LD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; NANO- PEPTIDE; CHAIN: C;	MAJOR HISTOCOMPATIBILITY COMPLEX LD; MAJOR HISTOCOMPATIBILITY COMPLEX, LD

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fa Blast	Verify score	PMF score	SEQIDOL D score	Compound	PDB annotation
1071	1mhc	A	24	299	0			156.53	MHC CLASS I ANTIGEN H2-M3; IMHC 6 CHAIN: A, B, D, E; IMHC 7 NONAPEPTIDE FROM RAT NADH DEHYDROGENASE; IMHC 12 CHAIN: C, F; IMHC 13	HISTOCOMPATIBILITY ANTIGEN/PEPTIDE MAJOR HISTOCOMPATIBILITY COMPLEX; IMHC 8 ND1; IMHC 15
1071	1mhc	A	25	296	0			170.11	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPTVLL); CHAIN: P, Q	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1071	1mhc	A	26	297	0	0.53	-1202.08		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPTVLL); CHAIN: P, Q	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1071	1q03	A	25	298	0			177.20	MHC CLASS I H-2D2 HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS D) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL INHIBITORY RECEPTOR, MHC-1, C-1TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/FOI D score	Compound	PDB annotation
1071	1qg3	A	26	298	0	0.42	-1202.08		MHC CLASS I H-2D2 HEAVY CHAIN; CHAIN: A; BETA-2; MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C; D	COMPLEX ONK RECEPTOR/MHC CLASS II H2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M, NK-CELL SURFACE GLYCOPROTEIN YEA48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY48, LY49
1071	1qg4	A	25	296	0			173.19	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-C*W4 CHAIN: A; BETA-2; MICROGLOBULIN; CHAIN: B; HLA-C*W4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (G)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1071	1qg4	A	26	297	0	0.43	-1202.08		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-C*W4 CHAIN: A; BETA-2; MICROGLOBULIN; CHAIN: B; HLA-C*W4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (G)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1071	1ime	A	11	183	8.4e-80			83.62	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*AV68 ITMC 3 COMPLETED WITH A DECA-MERIC PEPTIDE (EVAPPEYTHK) ITMC 4	IMMUNOGLOBULIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pa Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1071	2f6v	H	186	305	4.2e-08	0.18	-1202.08		IMMUNOGLOBULIN FAB 2F64 4	
									IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTIBODY 8ZGOW 3 ANTIBODY 8ZGOW 3 (H0H52-02.FAB) 2GOW 4	
1087	1a0x	A	356	548	4.2e-32	0.32	0.96		INTEGRIN ALPHA 2 BETA, CHAIN: A, B	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
1087	1a2z	A	358	516	4.2e-12	0.23	0.81		VON WILLEBRAND FACTOR, CHAIN: A, B	COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, DINTICLOTIDE BINDING FOLD
1087	1a0g		345	552	4.2e-54	0.16	0.16		A1 DOMAIN OF VON WILLEBRAND FACTOR, CHAIN: NULL	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
1087	1a0k	A	361	545	1.4e-31	0.37	0.42		INTEGRIN ALPHA-1, CHAIN: A, B	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
1087	1a2i	A	358	534	3.4e-14	0.10	0.55		INTEGRIN CHAIN: A, COLLAGEN, CHAIN: B, C, D	COLLAGEN ADHESION
1087	1a2i	A	361	534	1.4e-28	0.23	1.00		INTEGRIN CHAIN: A, COLLAGEN, CHAIN: B, C, D	COLLAGEN ADHESION
1087	1fns	A	355	549	7e-51	0.29	0.49		IMMUNOGLOBULIN NM4-1GG1, CHAIN: L, IMMUNOGLOBULIN NM4-1GG1, CHAIN: H, VON WILLEBRAND FACTOR, CHAIN: A, INTEGRIN, CHAIN: NULL	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IIA (A, ALPHA) BINDING 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN B, BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE CELL ADHESION PROTEIN A- DOMAIN INTEGRIN, CELL
1087	1fdo		361	542	4.2e-35	0.13	0.48		INTEGRIN, CHAIN: NULL	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMR score	SEQ/PSOL D score	Compound	PDB annotation
1087	1lfa	A	361	547	76-32	-0.04	0.46		CD11A; ILFA 5 CHAIN: A, B; ILFA 6	ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
1087	1qo5	A	361	543	5.6e-30	0.33	0.77		ALPHA1 BETA1 INTEGRIN; CHAIN: A; ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
1088	1ctu		6	675	1.4e-77			82.96	CYCLODEXTRIN GLYCOSYLTRANSFERASE; ICU 6 CHAIN: NULL; ICU 7	GLYCOSIDASE GYASE; ICU 8 THERMOSTABLE ICU 14
1088	1e43	A	9	484	9.8e-17			79.59	ALPHA-AMYLASE; CHAIN: A;	HYDROLASE HYDROLASE, AMYLASE FAMILY 13
1088	1gey	A	1	397	5.6e-18			74.07	GLUCAN 1,4-ALPHA- MALTOSE; CHAIN: A; MALTOSE; CHAIN: A;	HYDROLASE BETA-ALPHA- BARREL, BETA SHEET
1088	1bx0	A	5	488	5.6e-43			66.82	ALPHA AMYLASE (PPA); CHAIN: A;	HYDROLASE ALPHA-AMYLASE, INHIBITOR, CARBOHYDRATE, PANCREAS
1088	1qpo	A	12	671	4.2e-70			81.19	ALPHA-AMYLASE; CHAIN: A;	HYDROLASE "MALTODINIC" ALPHA AMYLASE, AMYLASE, GLYCOSIDE HYDROLASE, STARCH DEGRADATION
1088	1uok		110	675	0			90.36	OLIGO-1,6- GLUCOSIDASE; CHAIN: NULL;	GLYCOSIDASE GLUCOSIDASE, SUGAR DEGRADATION; HYDROLASE, TIM-BARREL 2
1088	1uok		7	543	0			74.70	OLIGO-1,6- GLUCOSIDASE; CHAIN: NULL;	GLYCOSIDASE GLUCOSIDASE, SUGAR DEGRADATION; HYDROLASE, TIM-BARREL 2



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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMR score	SEQPOL D score	Compound	PDB annotation
1090	1aab		675	754	1,4e-17	0.90	1.00		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN; NULL; 1AAB 6	GLYCOSIDASE, HYDROLASE DNA-BINDING HMGB DNA-BINDING HMGB-BOX DOMAIN A OF RAT HMGB; 1AAB 8 HMGB-BOX 1AAB 20
1090	1aab		676	754	1,7e-23	0.83	1.00		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN; NULL; 1AAB 6	DNA-BINDING HMGB DNA-BINDING HMGB-BOX DOMAIN A OF RAT HMGB; 1AAB 8 HMGB-BOX 1AAB 20
1090	1eg7	A	669	751	4,2e-25	0.51	1.00		NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA BINDING PROTEIN HMGB BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
1090	1ecl	A	680	748	1,4e-14	0.29	1.00		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-ID-CpCp*(DDO) CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA HMGB-1, AMPHOTERICIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
1090	1ecl	A	681	748	3,4e-20	0.47	1.00		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-ID-CpCp*(DDO) CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA HMGB-1, AMPHOTERICIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
1090	1hne		676	751	5,6e-29	0.50	1.00		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) DNA-BINDING 1HME 3 HMGB-BOX DOMAIN B OF RAT HMGB (NMR, 1 STRUCTURE) 1HME 4	GLYCOSIDASE, HYDROLASE DNA-BINDING HMGB DNA-BINDING HMGB-BOX DOMAIN A OF RAT HMGB; 1AAB 8 HMGB-BOX 1AAB 20
1090	1hem		679	752	2,8e-27	0.68	1.00		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) DNA-BINDING 1HME 3 HMGB-BOX DOMAIN B OF RAT HMGB (NMR, 1 STRUCTURE) 1HME 4	GLYCOSIDASE, HYDROLASE DNA-BINDING HMGB DNA-BINDING HMGB-BOX DOMAIN A OF RAT HMGB; 1AAB 8 HMGB-BOX 1AAB 20

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T.A.	END AA	Pt Blast	Verity score	PMF score	SRC/FOL. ID score	Compound	PDB annotation
									MOBILITY GROUP PROTEIN 1 (HMG) BOX 2, COMPLETED WITH HISM 3 MERCAPTOTRIANOL (NMR, MINIMIZED AVERAGE STRUCTURE) HISM 4	
1090	1qrv	A	678	752	1.4e-17	0.65	1.00		DNA (5'- 1d <sup>+</sup> Gp <sup>+</sup> Cp <sup>+</sup> Gp <sup>+</sup> Ap <sup>+</sup> Ap <sup>+</sup> *Tp <sup>+</sup> Cp <sup>+</sup> Gp <sup>+</sup> Cp <sup>+</sup> )-3'); CHAIN: C, D, HIGH MOBILITY GROUP PROTEIN D; CHAIN: A, B;	GENE REGULATION/DNA HMG-D; PROTEIN-DNA COMPLEX, HMG DOMAIN, NON-SEQUENCE SPECIFIC 2 CHROMOSOMAL PROTEIN HMG-D
1091	1d5s	B	342	382	5.6e-13			61.26	P1-ARG ANTITRYPSIN; CHAIN: A; P1-ARG ANTITRYPSIN; CHAIN: B;	HYDROLASE INHIBITOR SERPIN FOLD, RCL CLEAVAGE, A BETA SHEET POLYMERISATION
1091	1d5s	B	646	686	1.2e-14	-0.81	0.75		P1-ARG ANTITRYPSIN; CHAIN: A; P1-ARG ANTITRYPSIN; CHAIN: B;	HYDROLASE INHIBITOR SERPIN FOLD, RCL CLEAVAGE, A BETA SHEET POLYMERISATION
1091	1d5s	B	646	686	9.8e-13	-0.81	0.75		P1-ARG ANTITRYPSIN; CHAIN: A; P1-ARG ANTITRYPSIN; CHAIN: B;	HYDROLASE INHIBITOR SERPIN FOLD, RCL CLEAVAGE, A BETA SHEET POLYMERISATION
1091	1d2x	A	12	346	0			370.31	ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1- ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C; ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1- ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1- ANTITRYPSIN, 2 TRYPSIN
1091	1d2x	A	316	650	0			366.89	ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1- ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1- ANTITRYPSIN, 2 TRYPSIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1091	1exx	A	317	650	0	0.69	1.00		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1-ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR, PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYPSIN, 2 TRYPSIN
1091	1exx	B	651	686	1.1e-11	-0.78	0.30		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1-ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR, PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYPSIN, 2 TRYPSIN
1091	1exx	B	651	686	3.4e-12	-0.78	0.30		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1-ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR, PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYPSIN, 2 TRYPSIN
1091	1qjp	A	11	382	0			424.42	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR, ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTITRYPSIN, SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1091	1qjp	A	315	686	0			424.95	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR, ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTITRYPSIN, SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1091	1qjp	A	317	686	0	0.82	1.00		ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR, ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTITRYPSIN, SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEOPOL D score	Compound	PDB annotation
1091	1qmb	B	341	382	1.4e-12			61.02	ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	GLYCOPROTEIN SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION ACUTE PHASE
1091	1qmb	B	645	686	2.8e-12	-0.81	0.90		ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-PI, SERPIN, ANITRYPSIN, POLYMER, CLEAVED
1091	1qmb	B	645	686	5.1e-14	-0.81	0.90		ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-PI, SERPIN, ANITRYPSIN, POLYMER, CLEAVED
1092	1adl	A	330	536	1.4e-69	0.19	0.65		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-PI, SERPIN, ANITRYPSIN, POLYMER, CLEAVED
1092	1a01	A	330	530	1.4e-67	0.07	0.76		BET-A-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1092	1bnu	P	330	536	2.8e-69	0.21	0.49		ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1092	1adl	A	328	536	7e-70	0.32	0.93		PLASMINOGEN; CHAIN: A, B, C, D;	BLOOD CLOTTING PLASMINOGEN, CATALYTIC DOMAIN
1092	1dlc	A	339	430	2.8e-17	0.39	-0.09		COMPLEMENT FACTOR B; CHAIN: A, B;	HYDROLASE SERINE PROTEASE, COMPLEMENT SYSTEM, FACTOR B, PROTEIN-2, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1092	1dlc	A	476	534	1.3e-07	-0.21	0.21		COMPLEMENT FACTOR B, CHAIN: A, B <sub>1</sub>	INTERACTION, ACTIVATION MECHANISM, BETA-BARREL FOLD.
1092	1dlv	A	352	497	0.0034	0.17	0.89		COMPLEMENT C1S COMPONENT, CHAIN: A <sub>1</sub>	HYDROLASE TRYPSIN-LIKE SERIN PROTEASE, CCP (OR RUSHI OR SC5)MODULE
1092	1l7z	A	330	536	1.4e-67	0.34	0.95		TRYPSIN II, ANIONIC, CHAIN: A; PANCREATIC TRYPSIN INHIBITOR, CHAIN: I	HYDROLASE/HYDROLASE INHIBITOR BPTI SERINE PROTEASE, TRYPSIN PRECURSOR
1092	1fh8	A	331	497	0.0017	0.66	0.84		TRYPSIN, CHAIN: A; GLY-ALA-ARG, CHAIN: B <sub>1</sub>	HYDROLASE BETA BARREL
1092	1fhi	A	330	536	1.3e-71	0.09	0.77		TRYPSIN, CHAIN: A <sub>1</sub>	HYDROLASE SERINE PROTEASE, HYDROLASE
1092	1qdf	A	357	532	3.4e-09	0.41	0.19		EXFOLIATIVE TOXIN B, CHAIN: A <sub>1</sub>	HYDROLASE, TOXIN EPIDERMOLYTIC TOXIN B, SERINE PROTEASE, SUPERANTIGEN, HYDROLASE, TOXIN
1092	1slw	B	330	536	5.6e-67	0.29	0.60		ECOTIN, CHAIN: A; ANIONIC TRYPSIN, CHAIN: B <sub>1</sub>	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR, SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE-SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1092	1tm	A	330	536	1.4e-70	0.30	0.43		HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DISOPROPYL FLUOROPHOSPHOULO RIDATE (OPF) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	
1092	2sta		357	532	1.7e-13	0.47	0.62		SERINE PROTEINASE; CHAIN: NULL;	HYDROLASE HYDROLASE, SERINE PROTEASE
1092	2sta	E	330	534	1.4e-68	0.17	0.76		TRYPSIN; CHAIN: E; TRYPSIN INHIBITOR; CHAIN: I	HYDROLASE/HYDROLASE INHIBITOR SERINE PROTEINASE, TRYPSIN INHIBITOR
1092	5ppp		330	536	2.8e-65	0.09	0.51		BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
1103	1d2a	A	27	242	3.4e-39	0.45	0.78		ACID PHOSPHATASE; CHAIN: A;	HYDROLASE ALL ALPHA
1104	1cdq		36	112	2.8e-21			142.48	COMPLEMENT REGULATORY PROTEIN CD59 (NMR, 20 STRUCTURES) ICDQ 3	
1104	1cdy		59	166	1e-08	0.23	-0.14		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MIC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1104	1erg		36	105	1.4e-20			132.21	COMPLEMENT FACTOR HUMAN COMPLEMENT REGULATORY PROTEIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/FOL D score	Compound	PDB annotation
1104	1B97	A	1	89	1.4e-53			54.30	CD59 (EXTRACELLULAR IER3 REGION, RESIDUES 1-70) (NMR, RESTRAINED MINIMIZED IER4 AVERAGE STRUCTURE) IER5	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1104	1B97	A	65	274	8.4e-52			269.92	JUNCTION ADHESION MOLECULE, CHAIN: A <sub>1</sub>	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1104	1B97	A	67	272	8.4e-52	0.92	1.00		JUNCTION ADHESION MOLECULE, CHAIN: A <sub>1</sub>	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1104	1B97	A	67	274	3.4e-51	0.90	1.00		JUNCTION ADHESION MOLECULE, CHAIN: A <sub>1</sub>	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1104	1wio	A	75	312	6.8e-28	0.01	-0.18		T-CELL SURFACE GLYCOPROTEIN CD4 <sub>1</sub> CHAIN: A <sub>1</sub> B <sub>1</sub>	GLYCOPROTEIN CD4 <sub>1</sub> IMMUNOGLOBULIN FOLD, TRANSMEMBRANE
1105	1i5f	A	20	86	1.4e-29			87.22	ANOLIPROTEIN CII, CHAIN: A <sub>1</sub>	LIPID TRANSPORT APOLIPROTEIN, AMPHIPATHIC ALPHA HELIX
1105	1i5f	A	71	137	1.2e-30	-0.93	0.77		ANOLIPROTEIN CII, CHAIN: A <sub>1</sub>	LIPID TRANSPORT APOLIPROTEIN, AMPHIPATHIC ALPHA HELIX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1105	1h5j	A	71	137	1.2c-30			86.49	APOLIPOPROTEIN CII; CHAIN: A;	LIPID TRANSPORT APOLIPOPROTEIN-LIPID INTERACTION, AMPHIPATHIC ALPHA HELIX
1105	1h5j	A	71	137	7c-29	-0.93	0.77		APOLIPOPROTEIN CII; CHAIN: A;	LIPID TRANSPORT APOLIPOPROTEIN-LIPID INTERACTION, AMPHIPATHIC ALPHA HELIX
1106	1h6q	A	1	159	2.8c-60	0.40	1.00		TRANSLATIONALLY CONTROLLED TUMOR PROTEIN; CHAIN: A;	TUMOR-ASSOCIATED PROTEIN TCTP, P23FYF, TUMOR-ASSOCIATED PROTEIN, FUNCTION UNKNOWN
1106	1h6q	A	1	160	1.7c-58	0.37	1.00		TRANSLATIONALLY CONTROLLED TUMOR PROTEIN; CHAIN: A;	TUMOR-ASSOCIATED PROTEIN TCTP, P23FYF, TUMOR-ASSOCIATED PROTEIN, FUNCTION UNKNOWN
1107	1ave	B	300	393	0.00051	-0.29	0.29		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX TRANSCRIPTION REGULATION(DNA) GABP/ALPHA, GABP/ALPHA; COMPLEX REGULATION(DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1107	1blx	B	337	411	0.00034	-0.03	0.09		CYCCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX INHIBITOR PROTEIN/KINASE INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX INHIBITOR PROTEIN/KINASE
1107	1ldq	A	337	397	0.00051	0.15	0.64		PIYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fol Blast	Verify score	PMF score	SFQOL D score	Compound	PDB annotation
1107	1lhn	D	337	394	0.00083	-0.47	0.55		NE-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P90 SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D	TRANSCRIPTION FACTOR P65; P90; TRANSCRIPTION FACTOR, IKB/NFkB COMPLEX
1107	1mgo		337	394	0.00068	0.18	0.11		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1107	1mft	E	345	398	0.001	-0.25	0.84		NE-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P90; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1107	1yes	B	337	423	0.00017	-0.05	0.03		P53; CHAIN: A; 53BP2; CHAIN: B	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1108	1dth	A	108	240	1.4e-18	-0.26	0.06		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D	TRANSFERASE METHYLTRANSFERASE
1109	1a4		16	168	2.8e-26			99.38	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CING; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1109	1a4		97	222	2.8e-26	0.11	0.46		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CING; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN N/D	STAR T/A	END A/A	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1109	1ab8		3	74	5.6e-32			59.57	CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TRIC- DOMAIN, RESIDUES 1-75; CERIUM-LOADED, CALCIUM- BINDING PROTEIN
1109	1ap4		20	96	1.1e-18	0.79	1.00		CARDIAC N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING CNTG; CALCIUM-BINDING, REGULATION, TROPONIN C, CARDIAC MUSCLE 2 CONTRACTON
1109	1aut	B	18	179	2.8e-16			75.78	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCIUREGIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1109	1aws	A	1	76	2.8e-28			54.68	TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE CONTRACTON, CALCIUM- ACTIVATED TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
1109	1blq		1	78	8.4e-29			50.01	N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN SNTG, CALCIUM-BINDING, REGULATION, TROPONIN C, SKELETAL MUSCLE, 2 CONTRACTON
1109	1br1	B	26	166	1.3e-38	0.63	1.00		MYOSIN; CHAIN: A, B, C; D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
1109	1br1	B	26	166	1.3e-38			92.46	MYOSIN; CHAIN: A, B, C; D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
1109	1br1	B	97	209	1.4e-11	0.24	0.22		MYOSIN; CHAIN: A, B, C; D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
1109	1cdm	A	102	209	1.3e-29	-0.08	0.19		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PAM score	SEQFOL D score	Compound	PDB annotation
1109	1cdm	A	26	164	8.4e-59	0.72	1.00		CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
									CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3	
									CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
1109	1cdm	A	26	164	8.4e-59			118.25	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3	
									CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
									DEPENDENT PROTEIN KINASE II ICDM 4	
1109	1cll		102	209	9.8e-36	-0.05	0.24		CALCIUM-BINDING PROTEIN CALMODULIN (VERTERBATE) 1CLL 3	
1109	1cll		15	91	1.4e-19	0.39	1.00		CALCIUM-BINDING PROTEIN CALMODULIN (VERTERBATE) 1CLL 3	
1109	1cll		1	86	1.4e-42			50.32	CALCIUM-BINDING PROTEIN CALMODULIN (VERTERBATE) 1CLL 3	
1109	1cll		26	164	5.6e-65	0.73	1.00		CALCIUM-BINDING PROTEIN CALMODULIN (VERTERBATE) 1CLL 3	
1109	1cll		26	165	5.6e-65			135.44	CALCIUM-BINDING PROTEIN CALMODULIN (VERTERBATE) 1CLL 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1109	1cmf		15	87	1.4e-05			70.55	CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; ICMF 7 CALCIUM SATURATED CIB- CHAIN: A	CALCIUM-BINDING PROTEIN CALMODULIN APO TRAC-DOMAIN; ICMF 9 BLOOD CLOTTING HELICAL, EF-HANDS, BLOOD CLOTTING STRUCTURAL PROTEIN HELIX-TURN-HELIX
1109	1dgu	A	12	177	8.4e-16			64.07	CARDIAC TROPONIN C; CHAIN: A	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1109	1dli	A	20	165	2.8e-26			91.37	CARDIAC TROPONIN C; CHAIN: A	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1109	1dli	A	97	222	2.8e-26	0.36	0.63		CARDIAC TROPONIN C; CHAIN: A	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1109	1ecr	A	102	209	2.8e-33	0.04	0.29		CALMODULIN; CHAIN: A	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1109	1ecr	A	15	90	4.2e-18	0.29	0.95		CALMODULIN; CHAIN: A	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1109	1ecr	A	24	163	1.4e-62	0.75	1.00		CALMODULIN; CHAIN: A	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1109	1ecr	A	24	165	1.4e-62			132.92	CALMODULIN; CHAIN: A	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1109	1l4q	A	3	130	3.4e-10	-0.15	0.30		GRANCALCIN; CHAIN: A, B	METAL TRANSPORT PENT-A-EF-HAND PROTEIN, CALCIUM BINDING PROTEIN
1109	1fpw	A	48	216	8.4e-19	-0.21	0.37		CALCIUM-BINDING PROTEIN NCS-1; CHAIN: A	METAL BINDING PROTEIN YEAST PREQUEENIN EF-HAND, CALCIUM
1109	1fww	A	20	84	1.4e-05			67.19	CALMODULIN; CHAIN: A	METAL BINDING PROTEIN EF-FRAGMENT; CALCIUM, TRAC, C-2 TERMINAL DOMAIN, CALMODULIN
1109	1g8t	A	6	180	7e-14			65.19	NEURONAL CALCIUM SENSOR 1; CHAIN: A, B	METAL BINDING PROTEIN FREQUENIN; CALCIUM BINDING-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fol Blast	Verify score	PMF score	SPOFOL D score	Compound	PDB annotation
1109	legw	A	28	166	7e-11			89.53	CDCAp; CHAIN: A;	PROTEIN, EF-HAND, CALCIUM ION
1109	legv	A	15	203	2.8e-23			60.78	PROGRAMMED CELL DEATH PROTEIN 6; CHAIN: A;	APOPTOSIS PROBABLE CALCIUM-BINDING PROTEIN ALG-2, PENTAF-HAND PROTEIN, CALCIUM-BINDING PROTEIN
1109	legv	A	37	194	2.8e-23	0.19	0.24		PROGRAMMED CELL DEATH PROTEIN 6; CHAIN: A;	APOPTOSIS PROBABLE CALCIUM-BINDING PROTEIN ALG-2, PENTAF-HAND PROTEIN, CALCIUM-BINDING PROTEIN
1109	lilu		5	191	5.6e-11			58.57	RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN, CALCIUM-ANTIRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
1109	llef		102	224	7e-30	0.06	0.40		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION
1109	llef		17	165	7e-30			104.72	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, EF-HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1109	llep		102	224	2.8e-30	0.15	0.87		CONTRACTILE SYSTEM	CALCIUM-REGULATED MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, EF-HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Pst Blast	Verify score	PMF score	SEQEOL D score	Compound	PDB annotation
1109	1top		13	168	2.8e-30			107.77	PROTEIN TROPONIN C ITOP 3 CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1109	1trc	A	19	86	1.4e-05			63.97	CALCIUM BINDING PROTEIN CALMODULIN (TR-2)-CS FRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC 4	
1109	1trf		5	76	2.8e-28			53.23	MUSCLE PROTEIN TROPONIN C (TRIC FRAGMENT (APO FORM) (NMR 1 STRUCTURE) ITRF 3	
1109	1trk	A	102	209	2.8e-34	0.24	0.57		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1109	1trk	A	15	93	1.1e-18	0.39	0.99		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1109	1trk	A	23	166	9.8e-64	0.60	1.00		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1109	1trk	A	24	166	9.8e-64			133.11	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1109	1wdc	B	1	89	7e-20			67.20	SCALLOP MYOSIN; CHAIN: A, B, C <sub>1</sub>	SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1109	1wdc	B	26	168	1.7e-43			163.19	SCALLOP MYOSIN; CHAIN: A, B, C <sub>2</sub>	MUSCLE PROTEIN MYOSIN; CALCIUM BINDING PROTEIN; MUSCLE PROTEIN
1109	1wdc	B	26	168	5.6e-35	0.48	1.00		SCALLOP MYOSIN; CHAIN: A, B, C <sub>3</sub>	MUSCLE PROTEIN MYOSIN; CALCIUM BINDING PROTEIN; MUSCLE PROTEIN
1109	1wdc	B	28	166	1.7e-43	0.52	1.00		SCALLOP MYOSIN; CHAIN: A, B, C <sub>4</sub>	MUSCLE PROTEIN MYOSIN; CALCIUM BINDING PROTEIN; MUSCLE PROTEIN
1109	1wdc	C	26	169	1.3e-06			89.97	SCALLOP MYOSIN; CHAIN: A, B, C <sub>5</sub>	MUSCLE PROTEIN MYOSIN; CALCIUM BINDING PROTEIN; MUSCLE PROTEIN
1109	2mvs	B	1	90	2.8e-18			51.56	MYOSIN; CHAIN: A, B, C <sub>1</sub>	MUSCLE PROTEIN MYOSIN; SUBFRAGMENT-1; MYOSIN HEAD, 2 MOTOR PROTEIN
1109	2mvs	B	26	166	1.7e-38	-0.25	1.00		MYOSIN; CHAIN: A, B, C <sub>2</sub>	MUSCLE PROTEIN MYOSIN; SUBFRAGMENT-1; MYOSIN HEAD, 2 MOTOR PROTEIN
1109	2mvs	B	26	169	1.7e-38			146.55	MYOSIN; CHAIN: A, B, C <sub>3</sub>	MUSCLE PROTEIN MYOSIN; SUBFRAGMENT-1; MYOSIN HEAD, 2 MOTOR PROTEIN
1109	2mvs	B	7	78	5.6e-22			50.77	MYOSIN; CHAIN: A, B, C <sub>4</sub>	MUSCLE PROTEIN MYOSIN; SUBFRAGMENT-1; MYOSIN HEAD, 2 MOTOR PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1109	Zmgs	B	96	198	5.6e-17	-0.25	0.05		MYOSIN; CHAIN: A, B, C <sub>3</sub>	MUSCLE PROTEIN MUSCLE SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
1109	Zmgs	C	29	165	2.8e-35			87.97	MYOSIN; CHAIN: A, B, C <sub>3</sub>	MUSCLE PROTEIN MUSCLE SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
1109	Zmgs	C	32	165	2.8e-35	-0.05	1.00		MYOSIN; CHAIN: A, B, C <sub>3</sub>	MUSCLE PROTEIN MUSCLE SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
1112	1ajj		116	151	5.1e-09	-0.28	0.13		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: NULL.	RECEPTOR LR5, RECEPTOR LDL RECEPTOR, CYSTEINE-RICH MODULE, CALCIUM
1112	1ajj		117	151	5.6e-09	-0.06	0.01		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: NULL.	RECEPTOR LR5, RECEPTOR LDL RECEPTOR, CYSTEINE-RICH MODULE, CALCIUM
1112	18z	A	117	151	1.3e-07	-0.12	0.06		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A <sub>3</sub>	LIPID BINDING PROTEIN LDL RECEPTOR, LIGAND-BINDING DOMAIN, CALCIUM-BINDING, 2 FAMILIAL
1112	1ldl		116	151	5.1e-07	0.29	0.33		LOW-DENSITY LIPOPROTEIN RECEPTOR; LDL 4 CHAIN: NULL, LDL 5	BINDING PROTEIN LBI: LDL 7 LDL RECEPTOR CYSTEINE-RICH REPEAT LDL 15
1112	1afp		1	113	8.4e-07	0.35	0.04		ASFP; CHAIN: NULL.	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1112	1sfp		26	114	1.7e-10	0.37	0.09		ASFP; CHAIN: NULL;	PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
										SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
1112	1spp	A	26	112	8.5e-09	0.35	0.30		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-4; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-4; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SP)
1112	1spp	B	26	112	5.1e-10	0.17	0.11		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-4; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-4; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SP)
1119	1e1s	A	277	354	9.8e-07	0.46	-0.09		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A; CHAIN: B	SUGAR BINDING PROTEIN TDA; LECTIN, HEVENS POMAIN, UDA, SUPERANTIGEN
1119	9wga	A	485	655	4.2e-11	0.19	-0.19		LECTIN (AGGLUTININ) WHEAT GERM ISOLECTIN 2) 9WGA 3 LECTIN (AGGLUTININ) WHEAT GERM	
1119	9wga	A	915	1107	1.4e-13	0.04	-0.19			

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	P4 Bias	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1123	1a08	A	1	325	0			152.98	AGGLUTININ (ISOLECTIN 2) 9WGA.3	HYDROGENASE, HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX
1123	1lbe	L	1	325	0			137.95	FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L, M; SENSORY RHODOPHOSIN II; CHAIN: A <sub>1</sub>	HYDROGENASE, FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGEN 2 METABOLISM, PERPLASM
1124	1a08	A	199	326	5.6e-34	-0.18	0.33	86.06	ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A <sub>1</sub>	SIGNALING PROTEIN HEPATIC LECTIN III; C-TYPE LECTIN CRD
1124	1ag8	A	194	308	5.6e-28			100.53	NKG2-D; CHAIN: A <sub>1</sub>	PROLINE
1124	1byr	A	193	315	2.8e-26			94.69	NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B, A <sub>1</sub> MHC CLASS I CHAIN-RELATED PROTEIN A <sub>2</sub> CHAIN: C <sub>1</sub>	IMMUNE SYSTEM NKG2D, MIC-A, MIC, PERB11, ACTIVATING NK CELL RECEPTOR, NKG2D, C-TYPE, LECTIN LIKE, MIC-2 A, MIC-1 COMPLEX, IMMUNE SYSTEM
1124	1byr	A	48	163	1.4e-27				IMMUNE SYSTEM NKG2D, MIC-A, MIC, PERB11, ACTIVATING NK CELL RECEPTOR, NKG2D, C-TYPE, LECTIN LIKE, MIC-2 A <sub>1</sub>	

Table 5

SEQ NO:	PDB ID	CHAIN N/D	STAR T/A	END A/A	Est Blast	Verify score	PMF score	SRC/FOL D score	Compound	PDB annotation
1125	1z68	L	71	269	9.8e-17			73.24	RELATED PROTEIN A; CHAIN: C; ANTIBODY; CHAIN: L, H, M, P; 2B8 (IGG1-KAPPA-) 2B8 (IGG1-KAPPA-) ANTIBODY; CHAIN: L, H, M, P.	MHC-I, COMPLEX, IMMUNE SYSTEM IMMUNOGLOBULIN ANTIBODY IMMUNOGLOBULIN IMMUNOGLOBULIN
1125	1z68	L	83	267	9.8e-17	0.28	0.75			IMMUNOGLOBULIN IMMUNOGLOBULIN
1125	1adq	L	72	258	2.8e-22	0.38	1.00		IGG4 REA; CHAIN: A, RF- AN (GM/LAMBDA; CHAIN: H, L; IGG4 REA; CHAIN: A, RF- AN (GM/LAMBDA; CHAIN: H, L; IGG4 REA; CHAIN: A, RF- AN (GM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1125	1b2w	L	70	269	4.2e-20			73.56	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X- RAY STRUCTURE, THREE- DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
1125	1b6d	A	70	269	7e-21			73.38	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN, KAPPA LIGHT CHAIN DIMER, HEADER INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,
1125	1bth	A	2	362	1.3e-43	0.06	0.99		HEMOLIN; CHAIN: A, B;	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Fa Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1125	1bh	A	2	364	1.3e-43			121.44	HEMOLIN; CHAIN: A, B;	HOMOPHILIC ADHESION INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1125	1bh	A	73	386	5.1e-38	0.18	0.77		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1125	1bj	J	76	267	1.4e-21	0.10	0.89		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	HOMOPHILIC ADHESION IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1125	1bq	H	84	268	9.8e-14	0.01	0.34		COMPLEX (ANTIBODY/ANTIGEN) HYHEL-5 FAB COMPLEXED WITH BOBWHITE OVALB LYSOZYME IBOL 3	COMPLEX (ANTIBODY/ANTIGEN) HYHEL-5 FAB COMPLEXED WITH BOBWHITE OVALB LYSOZYME IBOL 3
1125	1bz	A	70	265	4.2e-19			73.01	ANTIBODY R24 (LIGHT CHAIN); CHAIN: A; ANTIBODY R24 (HEAVY CHAIN); CHAIN: B;	IMMUNE SYSTEM ANTIBODY (FAB FRAGMENT), IMMUNE SYSTEM
1125	1bc	A	83	267	5.6e-17	0.35	0.82		IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D; AZONIN-1; CHAIN: A;	IMMUNOGLOBULIN COMPLEX, IDIOTYPE, ANTI-IDIOTYPE
1125	1bc	A	10	363	5.6e-41	0.10	0.86		CELL ADHESION; NEURAL CELL ADHESION	CELL ADHESION; NEURAL CELL ADHESION

Table 5

SEQ ID No:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1125	1e66	A	15	364	1e-43			99.18	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1125	1e66	A	66	429	5.6e-40	0.19	0.76		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1125	1e66	A	72	379	1e-43	0.09	0.16		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1125	1e66	C	169	362	4.2e-38	0.15	0.48		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1125	1e66	C	6	167	8.4e-20	0.01	-0.09		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1125	1e66	C	81	270	4.2e-22	0.02	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1125	1e66	D	169	362	1.3e-39	0.32	0.80		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1125	1cvs	D	6	167	2.8e-20	-0.26	0.06		FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B, FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D,	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PAF, PGR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1125	1d5f	L	70	269	4.2e-21			72.82	CHIMERIC GERMALINE PRECURSOR OF OXY-COPE CHAIN: L; CHIMERIC GERMALINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNE SYSTEM, IMMUNE SYSTEM
1125	1db	L	70	269	8.4e-22			75.44	IMMUNOGLOBULIN 3D6 FAB IDPB 3	
1125	1db	L	76	267	8.4e-22	0.36	0.99		IMMUNOGLOBULIN 3D6 FAB IDPB 3	
1125	1dgt	R	58	362	3.4e-51			111.26	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1125	1dgt	R	75	362	3.4e-51	-0.21	0.46		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1125	1dgt	R	76	362	1.4e-39	-0.02	0.06		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMA score	SEQ/OL D score	Compound	PDB annotation
										RECEPTOR COMPLEX, VIRUS/ANTIBODY PROTEIN, RECEPTOR
1125	1epf	A	165	352	1.76-28	0.36	0.55		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D.	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1125	1epf	A	175	346	2.86-19	0.37	0.94		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D.	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1125	1epf	A	3	152	2.86-15	-0.07	0.00		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D.	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1125	1epf	A	72	272	4.26-24	-0.00	0.16		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D.	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1125	1ep2	B	170	362	2.86-34	0.04	0.23		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D. FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H.	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOLD FOLD
1125	1ep2	G	170	366	4.26-37	0.30	0.70		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D. FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H.	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOLD FOLD
1125	1ep4	C	169	362	2.86-39	0.03	0.51		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B, C, D. FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D.	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOLD FOLD
1125	1ep4	A	26	171	2.86-12	-0.13	0.07		HIGH AFFINITY	IMMUNE SYSTEM FC-REPSION RE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SRQPOL D score	Compound	PDB annotation
1125	1f6a	A	166	365	3.4e-27	0.26	0.18		IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	ALPHA: IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1125	1f6a	A	166	365	3.4e-27	0.26	0.18		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IGE EPSILON CHAIN C REGION; CHAIN: B, D	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1125	1f6a	A	171	346	1.4e-14	0.40	0.99		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IGE EPSILON CHAIN C REGION; CHAIN: B, D	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1125	1f6a	A	181	362	5.1e-26	0.27	0.11		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1125	1f6a	A	5	158	2.8e-12	-0.05	0.09		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1125	1f6a	A	77	265	4.2e-30	0.09	0.86		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1125	1f6a	A	170	362	8.5e-28	0.14	0.39		FC RECEPTOR FC(GAMMA)R1A; CHAIN: A;	IMMUNE SYSTEM MEMBRANE PROTEIN CD32, FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1125	1f6a	A	272	362	1.5e-17	0.48	0.74		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1125	1f8g	A	275	362	2.8e-17	0.38	0.72		TELOKIN; CHAIN: A	BARREL CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1125	1f8g	A	78	167	5.6e-13	0.02	0.53		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1125	1f6l	A	167	362	3.4e-26	0.21	0.01		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1125	1f6l	A	273	375	1.7e-16	0.34	-0.06		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1125	1g8k	A	167	356	6.8e-24	0.23	0.05		LEUCOCYTE IMMUNOGLOBULIN- LIKE RECEPTOR-1; CHAIN: A;	IMMUNE SYSTEM LEUCOCYTE INHIBITORY RECEPTOR-1; LEUCOCYTE IMMUNOGLOBULIN FOLD, 3-10 HELIX
1125	1f6l	L	83	267	9.8e-15	0.12	0.27		IDIOTYPIC FAB 790.1.4 (GGG) OF VIRUS IIA15 CHAIN: L, H, IIA17 ANTI-IDIOTYPIC FAB 409.5.3 (GGGA); IIA19 CHAIN: M, I IIA110	COMPLEX (IMMUNOGLOBULIN IGG1/IGGA)
1125	1f65	A	269	362	8.4e-18	-0.11	0.45		NEURAL CELL ADHESION MOLECULE; CHAIN: A;	CELL ADHESION N-CAM; INTERMEDIATE IMMUNOGLOBULIN FOLD
1125	1f65	A	272	363	6.8e-18	0.01	0.51		NEURAL CELL ADHESION MOLECULE; CHAIN: A;	CELL ADHESION N-CAM; INTERMEDIATE IMMUNOGLOBULIN FOLD
1125	1fll	G	164	366	6.8e-27	0.24	0.46		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, HHGF- 2, BASIC FIBROBLAST GROWTH

Table 5

SEQ ID NO:	PDB ID	CHAIN	STAR	END	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1125	1hh	G	170	366	1.4e-36	0.38	0.53		FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TYPE
1125	1hh	G	170	366	1.4e-36	0.38	0.53		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TYPE
1125	1hh	G	275	365	1.5e-16	0.61	0.55		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TYPE
1125	1hh	B	79	366	3.4e-37			82.33	INTERLEUKIN-1 BETA; CHAIN: A, TYPE I INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1125	Imco	H	1	363	9.8e-19			78.42	IMMUNOGLOBULIN (IGG1) (MCO) WITH A HINGE DELETION IMCO 3	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1125	Inf1	E	74	267	1.1e-21	0.32	0.56		N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL ID score	Compound	PDB annotation
1125	1osp	L	70	269	1.1e-17			75.72	FAB1841; CHAIN: L, H; OUTER SURFACE PROTEIN A; CHAIN: O;	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN N OSP A; COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN N, OUTER SURFACE 2 PROTEIN A COMPLEXED WITH FAB1841, BORRELIA BURGDORFERI 3 STRAIN B31)
1125	1vca	A	73	278	8.5e-27	0.57	0.93		HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A; B; 1VCA 5	CELL ADHESION PROTEIN VCAM-D1.2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
1125	1wio	A	76	442	1.5e-35			89.83	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A; B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1125	2dl	A	167	354	8.5e-23	0.17	0.00		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1125	2tcb	A	170	365	1.5e-27	-0.16	0.75		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1125	2tcb	A	278	375	1.5e-16	0.17	0.03		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1125	2tgv	L	76	267	1.1e-21	0.30	0.99		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2GROW 3 ANTIBODY 1H2 (H0H52-02; FAB) 2GROW 4	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	P3 Blast	Verify score	PMF score	SEQID score	Compound	PDB annotation
1125	Znct		282	363	1.5e-17	0.42	0.29		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
1125	3fct	A	73	269	1.4e-20			77.03	METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A, C, METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: B, D;	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT, IMMUNE 2 SYSTEM
1125	8ab	A	73	268	5.6e-23			74.31	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HLL) 8FAB 3	
1125	8ab	A	75	258	5.6e-23	0.42	1.00		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HLL) 8FAB 3	
1126	1b3u	A	22	571	4.5e-18	0.11	-1202.08		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1126	1e64	A	389	777	4.5e-21	0.55	-1202.08		KARYOPHERIN ALPHA; CHAIN: A, B, MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1126	1e5j	C	462	799	3e-15	0.02	-1202.08		BETA-CATENIN	TRANSCRIPTION BETA-

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1126	1l7w	A	462	915	1.5e-21	0.09	-1202.08		ARMADILLO REPEAT REGION; CHAIN: A, C, TC3-CBD (CATENIN BINDING DOMAIN); CHAIN: B, D	CATENIN, TC3, PROTEIN-PROTEIN COMPLEX
1126	1l7w	A	462	915	1.5e-21	0.09	-1202.08		BETA-CATENIN; CHAIN: A, C; ERTHELAL-CADHERIN; CHAIN: B, D	CELL ADHESION E-CADHERIN, E-CADHERIN, CELL ADHESION, BETA-CATENIN, PROTEIN-PROTEIN 2 COMPLEX, EXTENDED INTERFACE, ARMADILLO REPEAT, PHOSPHOSERINE
1126	1l7w	A	456	901	1.5e-18	0.14	-1202.08		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2
1126	1l7w	A	456	901	1.5e-18	0.14	-1202.08		ARMADILLO REPEATS, AUTONHIBITION, INTRASTERIC REGULATION	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1126	3bet		412	787	6e-17	0.11	-1202.08		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1127	1a7q	L	27	132	0.00012			60.18	MONOCLONAL ANTIBODY D13; CHAIN: L, H;	ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1127	1a7f	A	27	211	0.0015			61.80	ANTI-ID10TYPIC FAB 409.53 (IGG2A) FAB; CHAIN: A, B, L, H	ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1127	1b7w	A	25	133	0.00045			61.39	IG KAPPA CHAIN V4 REGION REI; CHAIN: A, B;	ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1127	1c7y		35	136	1.5e-09	0.41	-1202.08		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;

Table 5

SEQ ID NO.	PDB ID	CHAIN N ID	STAR TAA	END AA	P4 Blast	Verify score	PMF score	SIPQOL D score	Compound	PDB annotation
1127	1ae6	A	26	159	6e-08	0.25	-1202.08		AXONIN-1; CHAIN: A <sub>1</sub>	TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHG, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1127	1e0s	C	9	112	1.5e-11	0.04	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D <sub>2</sub>	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1127	1d49	A	37	134	4.5e-08	0.35	-1202.08		T LYMPHOCYTE ACTIVATION ANTIGEN; CHAIN: A <sub>1</sub>	IMMUNE SYSTEM B7.1 (CD80); IG SUPERFAMILY
1127	1eaj	A	28	132	7.5e-11	0.41	-1202.08		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B <sub>1</sub>	VIRUS/VIRAL PROTEIN RECEPTOR COXSACKIEVIRUS B-ADENOVIRUS RECEPTOR, HCAR, VIRUS/VIRAL PROTEIN RECEPTOR, IMMUNOGLOBULIN V DOMAIN FOLD, 2 SYMMETRIC DIMER
1127	1epf	A	31	112	6e-10	0.47	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D <sub>2</sub>	CELL ADHESION NCAM, NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1127	1e97	A	30	112	1.5e-10	0.12	-1202.08		JUNCTION ADHESION MOLECULE; CHAIN: A <sub>1</sub>	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1127	1e9m	L	27	210	3e-06			61.27	ENVELOPE GLYCOPROTEIN GP120; CHAIN: G, T-CELL SURFACE	VIRUS/VIRAL PROTEIN COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR, 2 ENVELOPE GP120

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PAM score	SEQID score	Compound	PDB annotation
1127	1hxm	B	32	142	6e-10	0.32	-1202.08		GLYCOPROTEIN CD4- CHAIN: C, ANTIBODY 17B, LIGHT CHAIN: CHAIN: L, ANTIBODY 17B, HEAVY CHAIN: CHAIN: H	FROM LABORATORY-ADAPTED ISOLATE, HX92, 3 SURFACE T- CELL GLYCOPROTEIN CD4, ANTIGEN-BINDING FRAGMENT 4 OF HUMAN IMMUNOGLOBULIN 17B
1127	1hgm	L	27	140	7.5e-05			60.22	IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) PV FRAGMENT 11GM.3	IMMUNE SYSTEM T-CELL RECEPTOR DELTA CHAIN; T- CELL RECEPTOR GAMMA CHAIN; IG DOMAIN, T CELL RECEPTOR, TCR, GPCR
1127	1hru		31	132	1.2e-09	0.36	-1202.08		MYELIN P0 PROTEIN; CHAIN: NULL;	STRUCTURAL PROTEIN MYELIN, STRUCTURAL PROTEIN, GLYCOPROTEIN, TRANSMEMBRANE, PHOSPHORYLATION, IMMUNOGLOBULIN FOLD, SIGNAL, MYELIN 2 MEMBRANE ADHESION MOLECULE
1127	1hkr		29	148	1.5e-09	0.16	-1202.08		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR, INHIBITORY RECEPTOR, NATURAL KILLER CELL, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1127	1vea	A	31	134	1.5e-10	0.22	-1202.08		HUMAN VASCULAR CELL ADHESION MOLECULE-1; TVCA 4 CHAIN: A, B, TVCA 5	CELL ADHESION PROTEIN VCAM-D1.2; TVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING TVCA 15
1131	1a25	A	648	768	1.4e-17	0.24	-1202.08		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1131	1a25	A	667	754	1.5e-18	0.08	-1202.08		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCULIN+/PHOSPHOLIPID BINDING PROTEIN 2 CALCULIN-BINDING PROTEIN
1131	1b9n	A	648	768	8.4e-23	0.21	-1202.08		SYNAPTOTAGMIN 1; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1131	1e9y	A	666	786	1.4e-08	0.16	-1202.08		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE C1A2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1131	1d9x	B	845	1047	2.8e-12	0.01	-1202.08		PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C; CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
1131	1day	A	647	781	5.6e-21	0.23	-1202.08		PROTEIN KINASE C; ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCULIN+/PHOSPHOLIPID BINDING PROTEIN, CALCULIN-BINDING 2
1131	1d9w		664	754	4.5e-19	0.04	-1202.08		PHOSPHOLIPASE A2; CHAIN: NDL1;	PHOSPHATIDYL-SERINE, PROTEIN KINASE C
1131	1d9w		666	765	2.8e-08	0.14	-1202.08		PHOSPHOLIPASE A2;	HYDROLASE C1A2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE, C2-DOMAIN, CALB DOMAIN



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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1131	1rsy		619	754	3e-20	0.22	-1202.08		CHAIN: NULL;	HYDROLASE, C2 DOMAIN, CALB DOMAIN
									CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN1 (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1131	1rsy		648	768	8.4e-23	0.11	-1202.08		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN1 (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1131	3rpb	A	650	779	9.8e-17	0.29	-1202.08		RABPHILIN-3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1133	1r88	A	54	378	1e-24			73.00	RHODOPSIN; CHAIN: A; B	SIGNALING PROTEIN- PHOTORECEPTOR, G PROTEIN- MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1133	1r88	B	54	371	3e-18			70.57	RHODOPSIN; CHAIN: A; B	SIGNALING PROTEIN- PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1133	1hne		6	81	1.1e-28			98.43	DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMG) (DNA-BINDING 1HME 3 HMG-BOX DOMAIN B OF KAT HMG) (NMRL 1 STRUCTURE) 1HME 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1133	1bim		9	87	1.1e-26			97.62	DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMG) BOX 2, COMPLEXED WITH HSM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) HSM 4	
1134	1b8	A	85	333	1.4e-47			73.96	GLYCEROL UPTAKE FACILITATOR PROTEIN; CHAIN: A;	MEMBRANE PROTEIN GLPF; GLYCEROL-CONDUCTING MEMBRANE CHANNEL, PROTEIN ALU DOMAIN SRP9/14, ALU BM, RBD, ALU DOMAIN, CRYSTAL STRUCTURE, RNA BINDING, SIGNAL 2 RECOGNITION PARTICLE (SRP), TRANSLATION REGULATION
1138	1914		1	104	9.8e-36			69.38	SIGNAL RECOGNITION PARTICLE 9/14 FUSION PROTEIN; CHAIN: NULL;	
1138	1dhp	A	35	327	1.4e-91	0.66	-1202.08		DIIHYDRODIPICOLINATE SYNTHASE; CHAIN: A; B;	SYNTHASE DHDP; SYNTHASE, DIIHYDRODIPICOLINATE
1138	1dhp	A	35	327	1.4e-91			130.43	DIIHYDRODIPICOLINATE SYNTHASE; CHAIN: A; B;	SYNTHASE DHDP; SYNTHASE, DIIHYDRODIPICOLINATE
1138	16k	A	10	304	1.4e-69			123.19	N- ACETYLEURAMINATE LYASE; CHAIN: A, C;	LYASE BETA BARREL, LYASE
1138	16k	A	33	327	3e-76			123.09	N- ACETYLEURAMINATE LYASE; CHAIN: A, C;	LYASE BETA BARREL, LYASE
1138	16k	A	34	318	3e-76	0.52	-1202.08		N- ACETYLEURAMINATE LYASE; CHAIN: A, C;	LYASE BETA BARREL, LYASE
1138	16k	A	34	323	5.6e-69	0.44	-1202.08		N-	LYASE BETA BARREL, LYASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1138	1nal	1	11	300	76-64			121.57	ACETYLEURAMINATE LYASE; CHAIN: A, C;	LYASE
1138	1nal	1	34	318	45-75	0.66	-1202.08		N- ACETYLEURAMINATE LYASE; 1NAL 4 CHAIN: 1, 2, 3, 4; 1NAL 5	LYASE
1138	1nal	1	34	319	1-46-63	0.61	-1202.08		N- ACETYLEURAMINATE LYASE; 1NAL 4 CHAIN: 1, 2, 3, 4; 1NAL 5	LYASE
1138	1nal	1	34	323	45-75			121.46	N- ACETYLEURAMINATE LYASE; 1NAL 4 CHAIN: 1, 2, 3, 4; 1NAL 5	LYASE
1140	1hcl	A	363	478	15-6-08	0.04	-1202.08		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN- BINDING PROTEIN
1142	1ak5	1	176	284	1-4-10	0.44	-1202.08		THROMBIN LIGHT CHAIN; CHAIN: A, B, C; D-THROMBIN HEAVY CHAIN; CHAIN: M, N, O P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR 1-GIU1-4GLV-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN, HGR, CMK, SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	Pst score	SEQ/OL D score	Compound	PDB annotation
1142	1dk5	I	252	353	5.6e-14	0.33	-1202.08		THROMBIN LIGHT CHAIN: A, B, C; D: THROMBIN HEAVY CHAIN: CHAIN: M, N, O, P: THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN: EGR-CNR SERINE PROTEINASE, EGR-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIHIBINOLYTIC COMPLEX
1142	1dk5	I	320	427	5.6e-12	0.33	-1202.08		THROMBIN LIGHT CHAIN: CHAIN: A, B, C; D: THROMBIN HEAVY CHAIN: CHAIN: M, N, O, P: THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN: EGR-CNR SERINE PROTEINASE, EGR-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIHIBINOLYTIC COMPLEX
1142	1dk7	A	214	288	1.4e-09	0.33	-1202.08		LDL RECEPTOR, CHAIN: A <sub>1</sub>	CELL SURFACE RECEPTOR CELL SURFACE RECEPTOR, CALCIUM-BINDING, EGR-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL <sub>1</sub> VLDL
1142	1dk7	A	368	427	1.3e-09	0.02	-1202.08		LDL RECEPTOR, CHAIN: A <sub>1</sub>	CELL SURFACE RECEPTOR CELL SURFACE RECEPTOR, CALCIUM-BINDING, EGR-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL <sub>1</sub> VLDL
1142	1dk6		163	288	5.6e-09	0.18	-1202.08		LAMININ: CHAIN: NULL; FACTOR IXA: CHAIN: G; D: PRP-PRO-ARG; CHAIN: I <sub>1</sub>	GLYCOPROTEIN ELICOPROTEIN COMPLEX (BLOOD COAGULATION/INHIBITOR)
1142	1dkx	L	250	327	8.3e-09	0.09	-1202.08		CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/BG, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEINASE	CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/BG, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEINASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Est Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1142	9wga	A	290	462	7e-15	0.01	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1142	9wga	A	98	263	2.5e-15	-0.00	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
1143	1888	A	1	275	7e-82			58.80	RHODOPSIN; CHAIN: A; B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1143	1888	A	25	366	1.4e-90			95.22	RHODOPSIN; CHAIN: A; B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1143	1888	B	23	352	2.5e-82			66.80	RHODOPSIN; CHAIN: A; B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1145	1agc	A	661	780	6e-23	0.03	-1202.08		XII; CHAIN: A; B; PEPTIDE; CHAIN: C; D	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE BINDING 2 MODULE, PTB DOMAIN
1145	1ddm	A	484	618	1.5e-13	0.11	-1202.08		NIMB PROTEIN; CHAIN: A; NIMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING PROTEIN/TRANSEASE/ NAC; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	P3 Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1145	1dnn	A	661	778	4.5e-25	0.45	-1202.08		NIMB PROTEIN-CHAIN: A; NIMB ASSOCIATE KINASE; CHAIN: B;	DOMAIN (PTB), ASYMMETRIC CELL DIVISION SIGNALING PROTEIN/TRANSPERASE NAK; COMPLEX SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMMETRIC CELL DIVISION
1145	1abc	A	477	620	9e-21	0.42	-1202.08		SHG; CHAIN: A; TRKA RECEPTOR PHOSPHOPEPTIDE; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), PHOSPHOTYROSINE 2 BINDING DOMAIN (PTB)
1145	1x11	A	661	782	3e-23	0.20	-1202.08		X11; CHAIN: A, B; 13-MER PEPTIDE; CHAIN: C, D;	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE), PTB DOMAIN
1145	2amb	A	661	786	7.5e-26	0.28	-1202.08		NIMB PROTEIN-CHAIN: A; GPPY PEPTIDE; CHAIN: B;	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMMETRIC CELL DIVISION
1148	1a25	A	224	347	4.2e-24	0.06	-1202.08		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1148	1a25	A	72	191	4.2e-24	0.15	-1202.08		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN N/D	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1148	1b9n	A	69	185	8.4e-30	0.21	-1202.08		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE.
1148	1dix	A	255	356	2.8e-21	0.32	-1202.08		PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C <sub>3</sub> CHAIN: A, B;	ENDOCYTOSIS/EXOCYTOSIS LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C <sub>3</sub> PHOSPHONOSITIDE-SPECIFIC
1148	1dix	B	115	355	1e-31	0.00	-1202.08		PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C <sub>3</sub> CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C <sub>3</sub> PHOSPHONOSITIDE-SPECIFIC
1148	1dix	B	255	356	2.8e-21	0.38	-1202.08		PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C <sub>3</sub> CHAIN: A, B;	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C <sub>3</sub> PHOSPHONOSITIDE-SPECIFIC
1148	1d9v	A	70	194	4.2e-26	0.20	-1202.08		PROTEIN KINASE C <sub>3</sub> ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++ PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLISERINE, PROTEIN KINASE C
1148	1d9w		240	331	1.5e-22	0.20	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fol Blast	Verify score	PMF score	SEQRES ID score	Compound	PDB annotation
1148	1tiw		90	181	8.4e-16	0.21	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	DOMAIN HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1148	3tpb	A	227	340	6e-24	0.05	-1202.08		RABPHILIN-3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAIN, C2B-DOMAIN, RABPHILIN
1148	3tpb	A	72	191	4.2e-20	0.10	-1202.08		RABPHILIN-3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAIN, C2B-DOMAIN, RABPHILIN
1149	1cex		8	53	0.0006	1.11	-1202.08		CUTINASE; CHAIN: NULL;	ENDOCYTOSIS/EXOCYTOSIS SERINE ESTERASE, GLYCOPROTEIN
1149	1kap	P	8	53	0.0015	1.00	-1202.08		ALKALINE PROTEASE; IKAP 4 CHAIN: P, IKAP 5 TETRAPEPTIDE (GLY SER ASN SER); IKAP 9 CHAIN: E, IKAP 10	ZINC METALLOPROTEASE P, AERUGINOSA ALKALINE PROTEASE, IKAP 6 CALCIUM BINDING PROTEIN IKAP 19
1149	1qpf	A	24	53	0.003	2.03	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1149	1eal		3	53	3e-05	1.40	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1149	1eal		3	70	0.003	0.91	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1149	1eal		8	63	0.00045	1.19	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE



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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1150	1eex		8	67	9e-06	1.25	-1202.08		CUTINASE; CHAIN: NULL;	PROTEINASE SERINE ESTERASE HYDROLASE, SERINE ESTERASE, CYCLOPROTEIN
1150	1gg6	A	8	67	0.0006	0.92	-1202.08		SERINE-CARBOXYL PROTEINASE; CHAIN: A; FRAGMENT OF TYROSTATIN; CHAIN: E;	HYDROLASE PSC, PSEUDOMONASPERSIN, PEPSTATIN-INSENSITIVE SERINE- CARBOXYL PROTEINASE
1150	1qq4	A	24	53	0.003	2.03	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1150	1tal		24	67	3e-05	1.57	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1150	1tal		3	63	3e-07	1.27	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1152	1r88	A	107	436	1.5e-15			61.82	RHODOPSIN; CHAIN: A; B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1152	1r88	B	107	434	4.5e-13			68.15	RHODOPSIN; CHAIN: A; B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1153	1etj	A	24	362	5.6e-52	0.54	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, G;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1153	1etj	A	480	761	1.4e-55	0.10	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1;	TRANSCRIPTION INHIBITOR BETA-PROPELLER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1153	1gt	A	725	931	2.8e-21	0.11	-1202.08		CHAIN: A, B, C; TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1153	1gt	A	72	431	4.2e-50	0.16	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1153	1gt	B	17	363	1.4e-58	0.36	-1202.08		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1153	1gt	B	513	802	1.1e-43	0.10	-1202.08		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1153	1gt	B	552	887	4.2e-34	0.10	-1202.08		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1153	1gt	B	644	936	2.8e-28	0.31	-1202.08		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	P4 Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
1158	1b6l	A	176	280	4.2e-57	0.22	-1202.08		RETROPEPSIN CHAIN: A, B;	SUBUNIT, COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETERODIMER 2 SIGNAL TRANSDUCTION
1158	1b6l	A	162	279	2.8e-17			55.92	ROUS SARCOMA VIRUS PROTEIN; CHAIN: A, B; INHIBITOR, CHAIN: C;	INHIBITOR HIV-1 P1 COMPLEX (ACID PROTEINASE/PEPTIDE) COMPLEX (PROTEASE/INHIBITOR) HUMAN IMMUNODEFICIENCY VIRUS PROTEIN, ROUS SARCOMA VIRUS 2 PROTEASE, CRYSTAL STRUCTURES, PROTEIN-MEDIATED INTERACTION, 3 VIRAL MATURATION, COMPLEX (PROTEASE/INHIBITOR) HEADER
1158	1b6l	A	1	111	1.4e-24			52.01	ROUS SARCOMA VIRUS PROTEIN; CHAIN: A, B; INHIBITOR, CHAIN: C;	COMPLEX (PROTEASE/INHIBITOR) HUMAN IMMUNODEFICIENCY VIRUS PROTEIN, ROUS SARCOMA VIRUS 2 PROTEASE, CRYSTAL STRUCTURES, PROTEIN-MEDIATED INTERACTION, 3 VIRAL MATURATION, COMPLEX (PROTEASE/INHIBITOR) HEADER
1158	1b6b	A	176	280	1.4e-60	0.15	-1202.08		HIV-1 PROTEINASE; CHAIN: A, B;	HYDROLASE HIV-1 PROTEINASE, HYDROLASE
1158	1e5x	A	176	280	2.8e-60	0.42	-1202.08		PROTEINASE; CHAIN: A, B; PEPTIDE INHIBITOR; CHAIN: A, B, HIV-1 PROTEINASE (RETROPEPSIN); CHAIN: C, D;	HYDROLASE HIV-1 PROTEINASE, HYDROLASE
1158	1d4z	C	176	280	5.6e-58	0.29	-1202.08			MUTANT, DIMER, INHIBITOR, OCCUPANCY
1158	1d4m		44	161	7.2e-23			57.26	DEOXYURIDINE 5'-	HYDROLASE DUTPASE, DUTP

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMR score	SEQPOL D score	Compound	PDB annotation
									TRIPHOSPHATE NUCLEOTIDOHYDROLASE; SE, CHAIN: NULL;	PYROPHOSPHATASE; HYDROLASE, DUTPASE, ELAV, TRIMERIC ENZYME, ASPARTYL PROTEASE
1158	1dm		58	150	7.5e-23	0.91	-1202.08		DEOXYURIDINE 5'- TRIPHOSPHATE NUCLEOTIDOHYDROLASE; SE, CHAIN: NULL;	HYDROLASE DUTPASE, DUTP PYROPHOSPHATASE; HYDROLASE, DUTPASE, ELAV, TRIMERIC ENZYME, ASPARTYL PROTEASE
1158	1dm		9	126	1.4e-18			56.78	DEOXYURIDINE 5'- TRIPHOSPHATE NUCLEOTIDOHYDROLASE; SE, CHAIN: NULL;	HYDROLASE DUTPASE, DUTP PYROPHOSPHATASE; HYDROLASE, DUTPASE, ELAV, TRIMERIC ENZYME, ASPARTYL PROTEASE
1158	1dmv	A	1	125	7e-22			61.05	DEOXYURIDINE 5'- TRIPHOSPHATE NUCLEOTIDOHYDROLASE; SE, CHAIN: A;	HYDROLASE DUTPASE, JELLY ROLL, MERCURY DERIVATIVE
1158	1dmv	A	32	160	4.5e-18			62.42	DEOXYURIDINE 5'- TRIPHOSPHATE NUCLEOTIDOHYDROLASE; SE, CHAIN: A;	HYDROLASE DUTPASE, JELLY ROLL, MERCURY DERIVATIVE
1158	1dmv	A	58	150	4.5e-18	0.76	-1202.08		DEOXYURIDINE 5'- TRIPHOSPHATE NUCLEOTIDOHYDROLASE; SE, CHAIN: A;	HYDROLASE DUTPASE, JELLY ROLL, MERCURY DERIVATIVE
1158	1fd	A	43	157	1.2e-22			62.82	POL. POLYPROTEIN; CHAIN: A, B;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA-BARREL
1158	1fd	A	58	150	1.2e-22	0.83	-1202.08		POL. POLYPROTEIN; CHAIN: A, B;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA-BARREL
1158	1fd	A	8	122	1.4e-21			62.45	POL. POLYPROTEIN; CHAIN: A, B;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA-BARREL
1158	1fd	A	43	180	1.5e-24			73.37	POL. POLYPROTEIN; CHAIN: A;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA-BARREL

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1158	1f7r	A	58	166	1.5e-24	0.29	-1202.08		POLYPROTEIN; CHAIN: A;	PROTEIN
1158	1f7r	A	8	136	2.8e-26			71.47	POLYPROTEIN; CHAIN: A;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA BARREL PROTEIN
1158	1fmb		176	280	2.8e-13			51.30	EA/V PROTEASE; CHAIN: NULL;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA BARREL PROTEIN
1158	1g6l	A	170	280	2.8e-63	-0.00	-1202.08		HIV-1 PROTEASE; CHAIN: A;	HYDROLASE HYDROLASE
1158	1g6l	A	93	280	2.8e-63			53.13	HIV-1 PROTEASE; CHAIN: A;	HYDROLASE HYDROLASE
1158	1hvc		148	280	1.4e-63	0.13	-1202.08		HYDROLASE/ACID PROTEASE HIV-1 PROTEASE (TETHERED DIMER LINKED BY IHVC 3 GLY-GLY-SER-SER-GLY) COMPLEXED WITH A-76928 IHVC 4	
1158	1hvc		60	280	1.4e-63			54.32	HYDROLASE/ACID PROTEASE HIV-1 PROTEASE (TETHERED DIMER LINKED BY IHVC 3 GLY-GLY-SER-SER-GLY) COMPLEXED WITH A-76928 IHVC 4	
1158	1hdc	A	176	279	2.8e-37	0.08	-1202.08		HYDROLASE/ACID PROTEINASE HUMAN IMMUNODEFICIENCY	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SKOPOL D score	Compound	PDB annotation
1158	1asp		176	280	14e-39	0.29	-1202.08		VIRUS TYPE 2 (HIV-2) PROTEINASE: IDA 3 COMPLEXED WITH THE INHIBITOR BIL A 1906 CONTAINING THE IDA 4	
									HYDROXYETHYLAMINE DIPEPTIDE ISOSTERE IDA 5	
									HYDROLASE/ACID PROTEINASE) SIMILAN IMMUNODEFICIENCY VIRUS (SIV) PROTEINASE 1SP 3(SIV MAC251.32H ISOLATE) (E.C.3.4.23.3) 1SP 4	
1167	1abq		18	281	8.5e-47	-0.33	0.06		BROMOPEROXIDASE A1; CHAIN: NULL;	HALOPEROXIDASE CHLOROPEROXIDASE A1; HALOPEROXIDASE A1; HALOPEROXIDASE, OXIDOREDUCTASE
1167	1a8s		16	280	14e-46	-0.21	0.11		CHLOROPEROXIDASE F; CHAIN: NULL;	HALOPEROXIDASE HALOPEROXIDASE F; OXIDOREDUCTASE, PROPIONATE COMPLEX
1167	1akx	A	13	270	3.4e-37	-0.33	0.03		2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIENOATE CHAIN: A;	HYDROLASE BPHD: HYDROLASE, PCB DEGRADATION
1167	1akx	A	6	282	3.4e-37			51.46	2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIENOATE CHAIN: A;	HYDROLASE BPHD: HYDROLASE, PCB DEGRADATION
1167	1eqw	A	13	281	1.2e-35	-0.34	0.01		HYDROLASE BPHD: HYDROLASE, PCB DEGRADATION	HYDROLASE A/B: HYDROLASE FOLD, DEHALOGENASE IS BOND

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1214	1ev2	B	26	110	3,40E-17	-0.29	0.09		CHAIN: A;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2, CHAIN: E; F, G, H;
1214	1ev2	G	26	110	3,40E-17	-0.61	0.05		FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2, CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2, CHAIN: E, F, G, H; FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2
1214	12eq	A	18	107	3,40E-18	0.04	0.93		HIGH AFFINITY IMMUNOGLOBULIN EPISILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RECEPTOR, IGE-BINDING 2
1214	1f6a	A	18	106	5,10E-17	0.31	0.9		HIGH AFFINITY IMMUNOGLOBULIN EPISILON RECEPTOR CHAIN: A; IGE-BINDING 2	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2
1214	1f6g	A	9	103	1,00E-17	-0.14	0.23		FC RECEPTOR FC(GAMMA)1A; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32, FC RECEPTOR, IMMUNOGLOBULIN, LEUCOCYTE, CD32
1214	1f6l	A	6	103	3,40E-16	-0.17	0.93		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR, BETA SANDWICH
1214	2f6b	A	9	105	8,50E-19	-0.14	0.17		FC GAMMA RUB; CHAIN: A;	IMMUNE SYSTEM CD32, RECEPTOR, FC, CD32, IMMUNE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL ID score	Compound	PDB annotation
1247	1ec4	A	130	442	1.4e-09	-0.03	0.88		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F.	SYSTEM
1247	1ec4	A	168	498	9.8e-12	0.33	1.00		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F.	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1247	1ia1	A	185	485	2.8e-11	0.11	0.95		IMPORTIN ALPHA; CHAIN: A.	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA, NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTONHIBITION, INTRASTERIC REGULATION
1247	2bc1		390	501	0.00011	0.23	0.25		BETA-CATENIN; CHAIN: NULL.	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-CATENIN, STRUCTURAL PROTEIN
1247	3bc1		224	505	8.4e-11	0.28	0.99		BETA-CATENIN; CHAIN: NULL.	ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1273	1hrs		2	278	1.7e-62			329.79	SULFUR-SUBSTITUTED RHODANSE; CHAIN: NULL.	TRANSFERASE, TRANSFERASE, RHODANSE.
1294	1dc5	I	104	218	5.10e-10	0.02	-0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR	SERINE PROTEINASE, COAGULATION FACTOR II, COAGULATION FACTOR II, FETOMODULIN T4, CD141 ANTIGEN, BCR-CHK SERINE PROTEINASE, BCR-LIKE DOMAINS, ANTICOAGULANT



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1294	1bxz		49	163	5.10E-08	0.01	-0.11		L-GILU-L-GILU-L-ARM; CHAIN: E, F, G, H; ANTISTASIN; CHAIN: NULL;	COMPLEX, 2 ANTIPIBRINOLYTIC COMPLEX SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN CRYSTAL STRUCTURE; FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1294	4m12		71	127	1.70E-09	0.25	-0.12		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4M12.3	
1301	1bx2	A	133	183	2.9e-07	-0.58	0.39		HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOMMUNITY, IMMUNE SYSTEM
1301	1eqk	A	132	182	4.3e-07	-0.56	0.05		CH3 DOMAIN OF MAK3 ANTIBODY; CHAIN: A, B;	IMMUNE SYSTEM CONSTANT DOMAIN, C1 SUBSET, IMMUNOGLOBULIN, IMMUNE SYSTEM
1301	1evs	C	79	133	0.00048	-0.01	0.04		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1301	1dgi	R	20	190	9.6e-16	-0.60	0.00		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PYR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Bias	Verify score	PMP score	SEOFOL D score	Compound	PDB annotation
1301	1duz	A	126	183	4.8e-07	-0.51	0.84		HLA-A*0201; CHAIN: A, D, BETA-2 MICROGLOBULIN, CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F.	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1301	1ek4	A	135	182	9.6e-08	-0.62	0.17		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B.	COMPLEX CD16, IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
1301	1f5w	A	32	131	9.6e-09	0.47	0.94		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B.	VIRUS/VIRAL PROTEIN RECEPTOR IMMUNOGLOBULIN V DOMAIN FOLD, SYMMETRIC DIMER
1301	1f5w	A	92	132	0.00032	-0.20	0.37		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B.	VIRUS/VIRAL PROTEIN RECEPTOR IMMUNOGLOBULIN V DOMAIN FOLD, SYMMETRIC DIMER
1301	1f62	D	135	182	1.4e-07	-0.48	0.40		IMMUNOGLOBULIN IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2.4	
1301	1hk	A	126	183	9.6e-08	-0.85	0.01		IMC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
1301	1neu		34	133	4.8e-06	0.38	0.03		MYELIN P0 PROTEIN; CHAIN: NULL;	STRUCTURAL PROTEIN MYELIN, GLYCOPROTEIN, TRANSMEMBRANE, PHOSPHORYLATION, IMMUNOGLOBULIN FOLD,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pst Blast score	Verify score	PMF score	SFOFOL D score	Compound	PDB annotation
1333	1ah	A	142	221	3.4e-27	-0.80	0.12		QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION; OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	SIGNAL, MYELIN 2 MEMBRANE ADHESION MOLECULE
1333	1ah	A	169	249	1.2e-29	0.01	0.88		QGRS ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION; OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1333	1b0g		385	480	0.0016	0.76	0.74		HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1333	1ney	C	141	221	1.7e-45	-0.46	0.03		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1ney	C	168	249	1.5e-48	-0.17	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1ney	C	196	277	5.1e-50	0.21	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1ney	C	224	305	8.5e-51	0.19	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1333	1mey	C	252	333	3.4e-51	0.40	1.00		FINGER PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1mey	C	252	333	3.4e-51	0.40	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1mey	C	252	334	3.4e-51			107.37	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1mey	C	308	389	5.1e-51	0.30	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1mey	C	336	415	8.5e-56	0.10	1.00		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1qtm	A	383	576	0.0002	0.23	0.28		PROLYL OLIGOPEPTIDASE; CHAIN: A;	HYDROLASE PROLYL ENDOPEPTIDASE, POST-PROLINE CLEAVING PROLYL OLIGOPEPTIDASE, AMNESIA, ALPHA/BETA-HYDROLASE, BETA-2 PROPELLER
1333	1h6	A	169	314	8.5e-58	-0.13	0.86		TEHUA: CHAIN: A, D, S; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1333	1H6	A	171	333	4e-69	0.03	0.92		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATON/DNA) COMPLEX (TRANSCRIPTION REGULATON/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1H6	A	196	366	6e-79			110.10	TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATON/DNA) COMPLEX (TRANSCRIPTION REGULATON/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1H6	A	197	342	5.1e-38	0.25	0.94		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATON/DNA) COMPLEX (TRANSCRIPTION REGULATON/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1H6	A	197	361	1.6e-78	-0.03	0.98		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATON/DNA) COMPLEX (TRANSCRIPTION REGULATON/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1H6	A	225	371	6.8e-39	0.23	1.00		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATON/DNA) COMPLEX (TRANSCRIPTION REGULATON/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pa Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1333	1t66	A	225	389	66-79	0.09	0.89		TH1A; CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1t66	A	253	389	1,76-36	0.22	1.00		TH1A; CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1t66	A	281	395	86-49	0.28	0.86		TH1A; CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1t66	A	281	471	1,46-32	-0.28	0.09		TH1A; CHAIN: A, D, S5 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1t66	C	143	249	3,46-33	-0.58	0.54		Y1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, Y1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	P4 Blast	Verify score	PMF score	SEOPOL D score	Compound	PDB annotation
1333	1ubd	C	171	277	8e-50	-0.10	0.98		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	1ubd	C	176	277	5.1e-35	-0.02	1.00		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	1ubd	C	194	306	2e-60			90.99	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	1ubd	C	222	333	2e-60	0.18	1.00		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	1ubd	C	232	333	3.4e-35	0.03	0.98		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOPOL D score	Compound	PDB annotation
1333	1ubd	C	278	389	8e-60	0.18	1.00		ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1333	1ubd	C	278	389	8e-60	0.18	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1333	1ubd	C	288	389	5.1e-35	0.28	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION) REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1333	2gi1	A	110	248	1.7e-34	-0.15	0.27		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING) PROTEIN/DNA) FIVE-FINGER GLI; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1333	2gi1	A	169	307	6e-64	0.12	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING) PROTEIN/DNA) FIVE-FINGER GLI; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1333	2gi1	A	176	304	1e-34	0.20	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING) PROTEIN/DNA) FIVE-FINGER GLI; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pa Blast	Verify score	PMF score	SRQPOL D score	Compound	PDB annotation
1333	2glt	A	196	335	4e-77			98.74	ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1333	2glt	A	196	363	4e-77	0.14	0.81		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1333	2glt	A	252	390	1e-76	0.36	0.94		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1333	2glt	A	260	388	3.4e-34	0.08	0.94		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1334	1aof	A	154	371	1.7e-24			55.32	GLUTATHIONE S-TRANSFERASE; CHAIN: A, B;	TRANSFERASE GST, GLUTATHIONE TRANSFERASE; TRANSFERASE, GLUTATHIONE CONJUGATION, DETOXIFICATION,
1334	1aw9		160	374	1.2e-42	0.03	0.72		GLUTATHIONE S-TRANSFERASE III; CHAIN: NDL1;	TRANSFERASE, HERBICIDE DETOXIFICATION
1334	1acd	A	160	366	5.1e-36	0.05	0.21		GLUTATHIONE S-TRANSFERASE I; CHAIN: A, B;	COMPLEX (TRANSFERASE/LIGAND) COMPLEX (TRANSFERASE/LIGAND),
1334	1aem	A	151	378	1e-36	0.22	0.23		LACTOYLGLUTATHION E; CHAIN: C, D	TRANSFERASE, HERBICIDE 2 DETOXIFICATION HEADER
1334	1aem	A							GLUTATHIONE S-TRANSFERASE; CHAIN: A;	TRANSFERASE GST, GLUTATHIONE CONJUGATING, PUTATIVE OXIDOREDUCTASE
1334	1aem	A	159	385	3.4e-38	0.09	0.75		GLUTATHIONE S-TRANSFERASE	TRANSFERASE, GLUTATHIONE S-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1334	1gsd	A	160	375	3.4e-35	0.09	0.86		TRANSFERASE YA CHAIN: A, B; GLUTATHIONE TRANSFERASE A1-1; 1GSD 5 CHAIN: A, B; 1GSD 6	TRANSFERASE, GLUTATHIONE
1334	1gse	A	160	385	1.7e-36	0.11	0.75		GLUTATHIONE TRANSFERASE; 1GSE 6 CHAIN: A, B; 1GSE 7	TRANSFERASE (GLUTATHIONE) A1-1 1GSE 19
1334	1hna		160	380	3.4e-37	0.20	0.80		TRANSFERASE (GLUTATHIONE) GLUTATHIONE S-TRANSFERASE (HUMAN, CLASS MU) (GSTM2-2) 1HNA 3 FORM A (E C.2.5.1.18) MUTANT WITH TRP 214 REPLACED BY PHE	
1334	1gsy	A	160	381	1.7e-37	0.04	0.33		1HNA 4 (V214P) 1HNA 5 MU CLASS GLUTATHIONE S-TRANSFERASE OF ISOENZYM CHAIN: A, B;	GLUTATHIONE TRANSFERASE RAT GST; GLUTATHIONE TRANSFERASE, ISOENZYME 3-3, T135 MUTANT
1348	1a0f	B	19	231	3.40E-70			88.97	FAB FRAGMENT, ANTIBODY ASB7; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT
1348	1a1f	H	258	443	1.70E-50	0.13	0		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL 1 CA, HIV CA, HIV P24, P24, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSIDIMMUNOGLOBULIN), HIV CAPSID PROTEIN 2 P24
1348	1a1f	H	15	230	5.10E-71	0.1	0.01		ANTI-IDIOTYPIC FAB	IMMUNOGLOBULIN

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	P4 Blast	Verify score	PMF score	SEQIDOL D score	Compound	PDB annotation
1348	1ba1	L	146	328	6.50E-16	-0.04	0.17		409.53 (GGGA) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN, C REGION, V REGION
1348	1ba1	L	146	328	6.50E-16	-0.04	0.17		IMMUNOGLOBULIN FAB FRAGMENT OF MURINE MONOCLONAL ANTIBODY AND2 COMPLEX 1BAF3 WITH ITS HAPTEN (2,2,6,6-TETRAMETHYL-1-PIPERIDINYOXY-1BAF 4 DINITROPHENYL) 1BAF 5	
1348	1b0	B	19	230	1.50E-67			80.18	CAMPATH-1G ANTIBODY; CHAIN: A, B, C, D, E, F, G, H	ANTIBODY ANTIBODY, FAB, CAMPATH-1G, CD52
1348	1b1	A	143	528	6.50E-26	0.01	0.7		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1348	1b1	A	44	443	1.40E-46			118.73	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1348	1b1	A	61	443	1.40E-46	0.23	0.57		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1348	1b1	B	15	232	1.70E-72	0.06	0.25		MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM
1348	1b1	B	19	231	1.70E-72			79.05	MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: B, D	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	P4 Blast	Verify score	PMF score	SEQID, D score	Compound	PDB annotation
1348	1d17	I	158	235	3,40E-19	0.35	0.64		A, C: MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D: IGG1 ANTIBODY 1696 (LIGHT CHAIN); CHAIN: I; IGG1 ANTIBODY 1696 (VARIABLE HEAVY CHAIN); CHAIN: H; IGG1 ANTIBODY 1696 (CONSTANT HEAVY CHAIN); CHAIN: I;	IMMUNE SYSTEM; IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1 FAB FRAGMENT, CROSS-REACTIVITY, HIV 1 PROTEASE, ENZYME 2 INHIBITION, IMMUNOGLOBULIN
1348	1d10	H	15	234	1,70E-72	-0.01	0.22		ASB7 MONOCLONAL ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN FRAGMENT
1348	1d10	H	19	233	1,70E-72			89.82	ASB7 MONOCLONAL ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN FRAGMENT
1348	1d12	H	19	233	3,40E-69			83.21	IGG1 FAB (IGG1, KAPPA); CHAIN: L, H;	IMMUNOGLOBULIN, FAB-FRAGMENT
1348	1d56	A	140	540	8,50E-38	0.02	0.49		AXONIN-1; CHAIN: A;	IMMUNOGLOBULIN, MRK96 FAB (IMMUNOGLOBULIN); GLYCOPROTEIN, TRANSMEMBRANE
1348	1d56	A	255	576	1,00E-30	-0.01	0.48		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1348	1d56	A	40	444	5,10E-63	0.36	0.86		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1348	1d58	C	137	341	3,40E-20	0.03	-0.01		FIBRINOLAST GROWTH FACTOR 2; CHAIN: A, B; FIBRINOLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGF-R, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEOPOL D score	Compound	PDB annotation
1348	1evs	D	137	341	1.40E-21	0.19	0.19		FIBROBLAST GROWTH FACTOR 2, CHAIN: A; B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FACTOR/GROWTH FACTOR RECEPTOR
1348	1d5i	H	258	454	6.80E-47	0.09	0.21		CHIMERIC GERM LINE PRECURSOR OF OXY-COPE CHAIN: I; CHIMERIC GERM LINE PRECURSOR OF OXY-COPE CHAIN: H; IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F;	IMMUNE SYSTEM IMMUNE SYSTEM
1348	1dee	A	143	327	5.10E-18	-0.09	0.01		IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM F4B-1BP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN F4B VHS 3 SPECIFICITY
1348	1dib	H	258	454	1.70E-47	-0.08	0.83		IMMUNOGLOBULIN 3D6 F4B 1DVB 3	
1348	1dib	L	143	327	1.00E-19	-0.04	0.16		IMMUNOGLOBULIN 3D6 F4B 1DVB 3	
1348	1dgi	R	23	340	8.20E-38	0.13	0.01		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS ELECTRON MICROSCOPY 2 POLIOVIRUS-RECEPTOR COMPLEX
1348	1dm2	A	247	437	1.20E-39	0.07	-0.18		IMMUNOGLOBULIN LAMBDA HEAVY	VIRUS/VIRAL PROTEIN, RECEPTOR IMMUNE SYSTEM FC GIG PHAGE DISPLAY PEPTIDE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Bias	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1348	1dd5	A	15	215	8.50E-58	0.23	-0.13		CHAIN: CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F	COMPLEX (ANTIBODY ANTIGEN)
									SCPV FRAGMENT 1P; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	1,4-BETA-N-ACETYLGLUCOSAMINASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT
1348	1dd5	A	256	425	3.40E-35	0.09	0.22		SCPV FRAGMENT 1P; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	1,4-BETA-N-ACETYLGLUCOSAMINASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT
1348	1dd5	C	137	341	1.70E-21	0.22	0.04		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR (GF); LIKE IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1, SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TYPE FOLD
1348	1dd5	H	258	444	1.70E-49	-0.17	0.11		IGG1 ANTIBODY 58.2 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 58.2 (HEAVY CHAIN); CHAIN: H; EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); CHAIN: P;	IMMUNE SYSTEM FAB 58.2; FAB 58.2; V3 LOOP; IMMUNOGLOBULIN FAB, HIV-1, GP120, V3, IMMUNE SYSTEM
1348	1dd5	H	258	440	1.50E-50	0.19	0.34		IMMUNOGLOBULIN FAB FRAGMENT FROM A MONOCLONAL ANTIBODY, ARSONATE ANTIBODY,	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1348	1fbi	H	258	440	1.70E-51	-0.06	0.12		R19.9 1FAI.3 (GGGB,K,APP) 1FAI.4 COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE MONOCLONAL ANTIBODY P913.7 (GGI) 1FBI.3 COMPLEXED WITH LYSOZYME (P.C.3.2.1.17) 1FBI.4	
1348	1fcg	A	237	443	4.10E-20	0.26	0.51		FC RECEPTOR PC(GAMMA)RLA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32, FC RECEPTOR, IMMUNOGLOBULIN, LEUCOCYTE, CD32
1348	1fkg	H	19	233	5.10E-67			79.18	IMMUNOGLOBULIN/VIR US HEMAGGLUTININ IGG2A FAB FRAGMENT (FAB 269) COMPLEXED WITH INFLUENZA VIRG 3 HEMAGGLUTININ HAI (STRAIN 347) (RESIDUES 101 - 108) 1FRG.4	
1348	1fvc	A	143	327	1.40E-17	-0.13	0.24		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD.3	
1348	1fvc	B	258	454	6.80E-48	0.02	0.59		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD.3	
1348	1fvi	B	19	233	6.80E-71			79.17	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 179) 1HII.3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	P4 Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1348	1he1	H	13	231	1.70E-68			80.32	ID10TYPIC FAB 790.14 (IGG1) OF VIRUS IIA15 CHAIN: L, H, IIA17 ANTI-ID10TYPIC FAB 400.53 (IGG2A), IIA19 CHAIN: M, L IIA110	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)
1348	1he2	H	16	235	1.40E-72	-0.02	0.07		COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC.5 PROTEIN G, STREPTOCOCCUS IIGC 15	
1348	1he3	H	258	444	3.40E-51	0.11	0.03		COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC.5 PROTEIN G, STREPTOCOCCUS IIGC 15	
1348	1he4	B	15	439	0	-0.02	0.13		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT REGION, IMMUNOGLOBULIN
1348	1he5	B	23	441	0			124.15	IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT REGION, IMMUNOGLOBULIN
1348	1he6	B	14	441	0			114.03	IGG1 INTACT ANTIBODY MAB61.13; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT REGION, IMMUNOGLOBULIN
1348	1he7	H	256	444	3.40E-51	0.04	-0.08		COMPLEX (ANTIBODY/IMMUNOSUP	IMMUNOGLOBULIN V REGION, C REGION, HINGE REGION



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	P4 Bias	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1348	1hb	B	143	443	2.90E-21	0.12	0.47		PRESSANT) IMMUNOGLOBULIN IGG1-KAPPA ANTIBODY FRAGMENT FAB COMPLEXED LIKE 3 WITH CYCLOSPORIN LIKE 4	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1348	1kel	H	19	230	1.20E-67			78.42	28B4 FAB; CHAIN: L, H;	
1348	1hl	A	148	336	1.00E-21	-0.08	0.19		LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN
1348	1lmk	A	16	215	1.50E-52	0.06	-0.13		ANTI- PHOSPHATIDYLINOSITOL SPECIFIC PHOSPHOLIPASE C DIABODY 11AK.3 SYNONYMS: L5MK16 DIABODY, SINGLE- CHAIN FV DIMER 11AK 4	
1348	1lmk	A	258	428	5.10E-53	0.1	0.34		IMMUNOGLOBULIN ANTI- PHOSPHATIDYLINOSITOL	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1348	Imco	H	147	527	5,10E-35	-0.24	0.09		1. SPECIFIC PHOSPHOLIPASE C DIABODY 1LMK 3 SYNONYMS: 15MK16 DIABODY, SINGLE- CHAIN PV DIMER 1LMK 4	
1348	Imco	H	147	527	5,10E-35	-0.24	0.09		1. IMAMINOGLUBULIN (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1348	Imco	H	18	437	8,50E-98	0.03	0.27		1. IMAMINOGLUBULIN (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1348	Imco	H	20	442	8,50E-98			101.92	1. IMAMINOGLUBULIN (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1348	Imcp	H	256	429	5,10E-35	0.29	0.51		1. IMAMINOGLUBULIN FRAGMENT (MCP/PC5603) 1MCP 4	
1348	Imfa		148	352	6,80E-24	0.24	0.09		1. IMAMINOGLUBULIN PV FRAGMENT (MURINE SE155-4) COMPLEX WITH THE TRISACCHARIDE: IMFA 3 ALPHA-D- GALACTOSE(1- 2)ALPHA-D- ABBOUS(1-3))ALPHA-	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fol Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									IMFA 4 D-MANNULOSE (PI-OM) (PART OF THE CELL-SURFACE CARBOHYDRATE IMFA 5 OF PATHOGENIC SALMONELLA) IMFA 6	
1348	Inca	H	15	233	5,10E-67			78.54	HYDROLASE; GLYCOSTYL; NO NEURAMINIDASE-NC4 (E.C.3.2.1.18) COMPLEX WITH FAB INCA 3	
1348	Incd	F	19	233	1,70E-70			83.51	N15 ALPHA-BETA T- CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
1348	Ingp	H	15	233	1,70E-73	0.1	0.12		N19 (GGI-LAMBDA-X) CHAIN: L, H	IMMUNOGLOBULIN
1348	Inqb	A	258	425	1,70E-33	0.02	0.69		SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C	IMMUNOGLOBULIN VARIABLE HEAVY (VD) DOMAIN; VARIABLE LIGHT (VD) ANTIBODY FRAGMENT; MULTIVALENT ANTIBODY; DIABODY; DOMAIN 2 SWAPPING; IMMUNOGLOBULIN
1348	Insk	H	258	438	6,80E-41	0.05	0.12		ANTIBODY; CHAIN: L, H	IMMUNOGLOBULIN FAB; GD2-GANGLIOSIDE; CARBOHYDRATE; MELANOMA; IMMUNOGLOBULIN
1348	Iqdc	H	16	233	6,80E-72	-0.09	0.12		ANTIBODY; CHAIN: H, L; PROTEIN G-PEPIDE; CHAIN: A; MAJOR OUTER MEMBRANE PROTEIN PL16; CHAIN: F	IMMUNE SYSTEM FAB; PORA; NEISSERIA MENINGITIDIS; PORIN
1348	Iqok	A	15	220	3,40E-56	0.04	-0.13		MPE-23 RECOMBINANT	IMMUNOGLOBULIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fol Blast	Verify score	PMF score	SEQ ID score	Compound	PDB annotation
									ANTIBODY FRAGMENT, CHAIN: A;	IMMUNOGLOBULIN, SINGLE-CHAIN PV, ANTI-CARCINOEMBRYONIC 2 ANTIGEN
1348	1q6k	A	256	430	1,70E-34	0.36	0.41		MFE-23 RECOMBINANT ANTIBODY FRAGMENT, CHAIN: A;	IMMUNOGLOBULIN, SINGLE-CHAIN PV, ANTI-CARCINOEMBRYONIC 2 ANTIGEN
1348	1t24	B	258	454	5.10E-45	0.24	0.3		IGG3-KAPPA ANTIBODY (LIGHT CHAIN); CHAIN: A; C; IGG3-KAPPA ANTIBODY (HEAVY CHAIN); CHAIN: B; D;	IMMUNE SYSTEM PRELIMINARY, IMMUNE SYSTEM
1348	1ab8	H	15	232	6.80E-72	0.23	0.54		MONOCLONAL ANTIBODY 3A2; CHAIN: H; L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
1348	1sb8	H	23	230	6.80E-72			80.32	MONOCLONAL ANTIBODY 3A2; CHAIN: H; L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
1348	1sb8	H	258	440	1.20E-50	-0.02	0.1		MONOCLONAL ANTIBODY 3A2; CHAIN: H; L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
1348	1am3	H	15	233	8.50E-73	-0.11	0		SM3 ANTIBODY; CHAIN: L; H; PEPTIDE EPTIOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPTIOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPTIOPE)
1348	1am3	H	23	233	8.50E-73			79.3	SM3 ANTIBODY; CHAIN: L; H; PEPTIDE EPTIOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPTIOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPTIOPE)
1348	1et	H	20	233	1.00E-65			78.05	IMMUNOGLOBULIN IGG1, MONOCLONAL, FAB FRAGMENT (1E33)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Est Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1348	1vbp		15	141	1.20E-47	0.11	-0.19		COMPLEX WITH CHOLERA 11ET3 TOXIN PEPTIDE 3 (CTT3) 11ET 4 VH-PS; CHAIN: NULL.	IMMUNOGLOBULIN NMR, VH DOMAIN, ANTIBODY, HUMAN, IMMUNOGLOBULIN
1348	1vto	A	98	428	8.20E-14	0.02	0.13		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, LIPOPROTEIN, POLYMERISM
1348	2568	L	146	328	1.00E-15	0.01	-0.01		IGG 3CS; CHAIN: L, H;	CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
1348	2f64	H	258	453	6.80E-47	-0.01	0.33		IMMUNOGLOBULIN 2F64 4	
1348	2f6j	H	256	429	1.70E-34	0.19	0.62		IMMUNOGLOBULIN IGF-A FAB FRAGMENT (G539) (GALACTAN-BINDING) 2F6J 3	
1348	2g2b	B	16	233	1.20E-73	0.09	0.53		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (G2ND6) 2G2B 3	
1348	2h1p	H	256	440	6.80E-53	-0.14	0.07		ZH1; CHAIN: L, H; PA1; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE) ANTIBODY STRUCTURE, CRYPOTOCOCUS, PEPTIDE, PHAGE LIBRARY, 2 POLYSACCHARIDE, COMPLEX (ANTIBODY/PEPTIDE)
1348	6f6b	H	258	444	6.80E-50	-0.07	0.06		IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT OF THE MORINE ANTI-	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMR score	SEOFOL D score	Compound	PDB annotation
									PHENYLARSONATE, 6FAB 3 ANTIBODY 36-71, FAB 36-71 6FAB 4	
									IMMUNOGLOBULIN FAB FRAGMENT BROM	
1348	86ab	A	148	336	3.40E-21	0.17	0.29		HUMAN IMMUNOGLOBULIN IGg1 (LAMBDA, H1D) 8FAB 3	
									2E8 (IGG1-KAPPA=) ANTIBODY; CHAIN: L, H, M, P	IMMUNOGLOBULIN IMMUNOGLOBULIN
1356	1268	L	22	222	1.7E-17			74.09	IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B	IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMANINE
	1aej	L	22	222	1.5E-19			73.51	FAB FRAGMENT; ANTIBODY ASPT; CHAIN: A, B, C, D	IMMUNOGLOBULIN, FAB FRAGMENT
1356	1ae0	A	29	222	3.4E-22	0.15	0.35		IGG4 REA; CHAIN: A; RE-ANTIGEN/LAMBDA; CHAIN: H, L	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN, RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
	1aeq	L	25	224	1.4E-26			71.74	IGG4 REA; CHAIN: A; RE-ANTIGEN/LAMBDA; CHAIN: H, L	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN, RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1356	1aeq	L	28	219	1.4E-26	0.09	0.78		IGG4 REA; CHAIN: A; RE-ANTIGEN/LAMBDA; CHAIN: H, L	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN, RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
	1ae2w	L						74.84	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN, IMMUNOGLOBULIN ANTIBODY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1356	1b2w	L	29	222	1.4e-22	0.10	0.80		CHAIN; CHAIN: H;	ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2X-RAY STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
									ANTIBODY (LIGHT CHAIN); CHAIN: L;	IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2X-RAY STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
									ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODIES, 2 FAB, X-RAY STRUCTURES, GAMMA-INTERFERON
1356	1b6f	L	29	222	1.2e-21	-0.07	0.31		ANTIBODY; CHAIN: L, H;	ANTIBODY ENGINEERING ANTIBODY ENGINEERING HUMANIZED AND CHIMERIC ANTIBODIES, 2 FAB, X-RAY STRUCTURES, GAMMA-INTERFERON
1356	1b6d	A	22	222	1.7e-22			74.61	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
1356	1b6d	A	29	222	1.7e-22	-0.03	0.69		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
1356	1b6j	L	22	222	1e-19			80.38	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
									IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
									IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
1356	1b6h	A	21	394	1.5e-55			115.28	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pa Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
1356	1bh	A	28	395	1.5e-55	0.01	0.07		HEMOLIN; CHAIN: A, B;	HOMOPHILIC ADHESION INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1356	1bj1	L	22	222	1.4e-22			72.47	FAB FRAGMENT; CHAIN: L, H, I, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
1356	1bj1	L	29	222	1.4e-22	0.02	0.39		FAB FRAGMENT; CHAIN: L, H, I, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
1356	1bng	A	22	222	3.4e-19			73.26	ANTIBODY (CB 4-1); CHAIN: A, B; PEPTIDE; CHAIN: C;	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY CROSS REACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1, COMPLEX (ANTIBODY/PEPTIDE)
1356	1bz7	A	22	218	3.4e-18			74.03	ANTIBODY R24 (LIGHT CHAIN); CHAIN: A; ANTIBODY R24 (HEAVY CHAIN); CHAIN: B;	IMMUNE SYSTEM ANTIBODY (FAB FRAGMENT), IMMUNE SYSTEM
1356	1cdy		135	315	6.3e-23	0.35	0.64		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1356	1cd1	L	22	222	1.2e-21			72.17	CAMPATH-1HLIGHT CHAIN; CHAIN: L;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52



Table 5

SEQ ID No.	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SR/OPL D score	Compound	PDB annotation
									CAMPATH-HHEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	
1356	1c66	A	26	395	1.7e-58	0.23	0.55		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1356	1c66	C	122	315	1.2e-42	0.32	0.52		FIBROBLAST GROWTH FACTOR 2; CHAIN: A; B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C; D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGR, PGR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1c66	C	240	395	1.7e-35	0.07	-0.18		FIBROBLAST GROWTH FACTOR 2; CHAIN: A; B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C; D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGR, PGR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1c66	C	29	120	6.8e-13	-0.07	0.03		FIBROBLAST GROWTH FACTOR 2; CHAIN: A; B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C; D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGR, PGR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1c66	C	34	223	1.4e-28	0.03	0.10		FIBROBLAST GROWTH FACTOR 2; CHAIN: A; B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C; D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR PGR, PGR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1c66	D	122	315	1.2e-42	0.28	0.47		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T.AA	END AA	Pst Blast	Verify score	PMF score	SEROFL D score	Compound	PDB annotation
									FACTOR 2, CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D <sub>2</sub>	FACTOR RECEPTOR FGF, FGF-R, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1cvs	D	240	395	3.4e-37	0.16	-0.14		FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D <sub>2</sub>	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGF-R, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1cvs	D	29	120	1e-11	-0.14	0.33		FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D <sub>2</sub>	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGF-R, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
									FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D <sub>2</sub>	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGF-R, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1cvs	D	34	223	1e-26	-0.12	0.37		FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D <sub>2</sub>	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGF-R, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
									CHIMERIC GERM LINE PRECURSOR OF OXY-COPE CHAIN: L <sub>1</sub> ; CHIMERIC GERM LINE PRECURSOR OF OXY-COPE CHAIN: H <sub>1</sub>	IMMUNE SYSTEM IMMUNE SYSTEM
1356	1dci	L	29	222	3.4e-22	-0.08	0.65		IGM RF 2A2, CHAIN: A, C, B; IGM RF 2A2, C, B	IMMUNE SYSTEM FAB-IP COMPLEX CRYSTAL STRUCTURE

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T, AA	END AA	P4 Blast	Verify score	PMF score	SECOPOL D score	Compound	PDB annotation
1356	1db	L	22	222	1.2e-21			76.72	CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H; IMMUNOGLOBULIN 3D6 FAB 1DB3	2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
1356	1dgi	R	29	315	5.1e-43	-0.29	0.27		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: I; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4; RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVA, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS- RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1356	1epf	A	118	305	4.2e-28	0.47	0.63		NEUTRAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1356	1epf	A	128	299	5.1e-22	0.34	1.00		NEUTRAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1356	1epf	A	235	379	1.7e-21	0.05	-0.09		NEUTRAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1356	1epf	A	27	225	5.1e-26	0.25	0.11		NEUTRAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1356	1ep2	E	123	315	6.8e-39	-0.11	0.05		FIBRINOGEN GROWTH FACTOR 2; CHAIN: A, B; C, D; FIBRINOGEN GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TYPE FOLD
1356	1ep2	E	240	395	1.5e-33	0.06	-0.17		FIBRINOGEN GROWTH FACTOR 2; CHAIN: A, B; C, D; FIBRINOGEN GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG) LIKE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Est Blast	Verify score	PMR score	SEQ/OL D score	Compound	PDB annotation
									GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H	DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREPOIL FOLD
1356	1e2	E	34	223	6.5e-24	0.24	0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREPOIL FOLD
1356	1e2	G	123	319	8.5e-43	0.29	0.23		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREPOIL FOLD
1356	1e2	G	240	395	1.7e-26	0.10	-0.07		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREPOIL FOLD
1356	1e2	G	29	124	1.7e-11	-0.03	0.24		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREPOIL FOLD
1356	1e2	G	34	223	1e-24	0.14	0.42		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG)-LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREPOIL FOLD
1356	1e2	C	122	315	1.7e-41	0.23	0.19		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1;

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T.AA	END AA	P4 Blast	Verify score	PMF score	SCOP/FOLD score	Compound	PDB annotation
1356	1evr	C	29	120	1.7e-11	-0.08	0.10		FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D <sub>1</sub>	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1evr	C	29	120	1.7e-11	-0.08	0.10		FIBROBLAST GROWTH FACTOR I; CHAIN: A, B <sub>1</sub> FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D <sub>1</sub>	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFRL1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1evr	C	34	223	5.1e-25	-0.07	0.22		FIBROBLAST GROWTH FACTOR I; CHAIN: A, B <sub>1</sub> FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D <sub>1</sub>	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFRL1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	12qa	A	119	318	2.1e-19	0.18	0.35		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A <sub>1</sub>	IMMUNE SYSTEM EC-EPSILON R-ALPHA; IMMUNOGLOBULIN FOLD, GELFOURPROTEIN, RECEPTOR, IGB-BINDING 2
1356	16eg	A	123	315	6.5e-23	0.23	0.55		FC RECEPTOR FC(GAMMA)BIL4; CHAIN: A <sub>1</sub>	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1356	16eg	A	228	395	3.4e-18	0.02	-0.19		FC RECEPTOR FC(GAMMA)BIL4; CHAIN: A <sub>1</sub>	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1356	16eg	A	225	315	8.5e-18	0.25	0.94		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1356	16eg	A	31	120	3.4e-14	0.14	0.30		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END AA	Pos Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
1356	1fcd	A	22	222	3.4e-22			73.26	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 LPVD 3	BARREL
1356	1fcd	A	29	222	3.4e-22	0.12	0.55		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 LPVD 3	
1356	1ge1	L	22	222	3.4e-21			73.99	ENVELOPE PROTEIN GP120-CHAIN-G, CD4-CHAIN-C, ANTIBODY 17B, CHAIN: L, H.	COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120, T-CELL SURFACE GLYCOPROTEIN CD4, 3 ANTIGEN-BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4 GLYCOSYLATED PROTEIN
1356	1hng	A	135	317	4.2e-26	0.32	0.03		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAV) IHNG 3	
1356	1igt	B	23	393	1e-18			74.95	IGGA INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN COMPLEX
1356	1hb	B	145	393	5.1e-19	-0.07	0.09		INTERLEUKIN-1 BETA, CHAIN: A, TYPE 1 INTERLEUKIN-1 RECEPTOR, CHAIN: B;	(IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR) COMPLEX
1356	1hb	B	32	319	2.1e-24			81.96	INTERLEUKIN-1 BETA.	COMPLEX

Table 5

SFPQ ID NO.	PDB ID	CITAI NID	STAR TAA	END AA	Fd Blast	Verify score	PMF score	SECFOL D score	Compound	PDB annotation
									CHAIN: A; TYPE I INTERLEUKIN-1 RECEPTOR; CHAIN: B;	(IMMUNOGLOBULIN)RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (MMUNOGLOBULINRECEPTOR)
I356	Hhb	B	34	315	2.1e-24	0.04	0.06		INTERLEUKIN-1 BETA; CHAIN: A; TYPE I INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN)RECEPTOR IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULINRECEPTOR)
									TYTTCIHN; CHAIN: NULL;	KINASE KINASE, TYTTCIHN INTRASTERIC REGULATION
I356	Lkca	A	26	120	1.7e-11	-0.35	0.12		LAMBDA III BENGE JONES PROTEIN CLE; CHAIN: A; B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENGE JONES PROTEIN
I356	Hlll	A	28	219	1.7e-25	0.24	0.98		IMMUNOGLOBULIN G1 (GGG) (MCG) WITH A HINGE DELETION IMCO 3	
I356	Hmeo	H	10	395	8.5e-25			83.75	IMMUNOGLOBULIN G1 (GGG) (MCG) WITH A HINGE DELETION IMCO 3	
I356	Hmco	H	25	384	8.5e-25	-0.18	0.33		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (GGG) (MCG) WITH A HINGE DELETION IMCO 3	MUSCLE PROTEIN CONNECTIN, NEXTJES; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
I356	Inet		226	315	1.1e-17	0.40	0.16		TYTTHN; CHAIN: NULL;	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1356	1nct		29	121	1.5e-14	0.11	0.05		TTIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXIN5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1356	1nfd	E	27	220	5.1e-25	0.38	0.74		N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D, H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
1356	1oep	L	22	222	1.7e-16			76/74	FAB 184.1; CHAIN: L, H; OUTER SURFACE PROTEIN A; CHAIN: O;	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN) OSFA; COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN) OUTER SURFACE 2 PROTEIN A COMPLEXED WITH FAB184.1, BORRELLIA BURGDORFERI 3 STRAIN B31
1356	1um		29	121	1.5e-14	-0.03	0.18		MUSCLE PROTEIN TTIN MODULE M5 (CONNECTIN) ITNM 3 (NMK, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
1356	2lbb	A	228	395	3.4e-18	0.01	-0.18		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1356	2lbb	A	28	191	8.5e-14	-0.28	0.01		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1356	2lhw	L	29	222	5.1e-23	-0.07	0.29		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION	



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									OF THE ANTI-CD18 2PGW 3 ANTIBODY #52 (FHH52-OZ EAB) 2PGW 4 NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN
1356	2acm		27	120	3.4e-12	0.21	0.36			1: CELL ADHESION GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
1356	36ct	A	22	222	1.7e-21			77.52	METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A; C; METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: B, D;	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT, IMMUNE 2 SYSTEM
1356	86db	A	26	221	8.5e-29			73.89	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HLL) 8FAB 3	
1356	86db	A	28	219	8.5e-29	0.18	0.94		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HLL) 8FAB 3	
1367	1b1i	A	29	129	4.2e-30	-0.05	0.76		HYDROLASE ANGIOGENIN; CHAIN: A; 8FAB 3	HYDROLASE HYDROLASE (VASCULARIZATION)
1367	1b6v	A	21	132	1.7e-43			50.95	RIBONUCLEASE; CHAIN: A, B;	MOLECULAR EVOLUTION MOLECULAR EVOLUTION, RIBONUCLEASE
1367	1b6v	A	27	132	1.7e-43	-0.27	0.98		RIBONUCLEASE; CHAIN: A, B;	MOLECULAR EVOLUTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1367	1brt	A	27	132	5.1e-42	-0.47	0.66		A, B;	MOLECULAR EVOLUTION, RIBONUCLEASE
									HYDROLASE/PHOSPHO RIC DIESTER RNA RIBONUCLEASE (BOVINE, SEMINAL) (BS-RNASE) HSR 3 RIBONUCLEASE A;	
1367	1dy5	A	27	132	3.4e-44	0.16	0.93		CHAIN: A, B;	HYDROLASE (PHOSPHORIC DIESTER) RIBONUCLEASE, DEAMINATION, ULTRA-HIGH RESOLUTION
1367	1gnt	A	24	132	3.4e-41	-0.11	1.00		EOSINOPHIL CATIONIC PROTEIN; CHAIN: A;	RIBONUCLEASE RIBONUCLEASE 3, RNASE 3 EOSINOPHIL, RIBONUCLEASE, CYTOTOXICITY
1367	1tdt		41	132	1.7e-39	-0.51	0.88		HYDROLASE/PHOSPHO RIC DIESTER RNA RIBONUCLEASE S (EC3.1.27.5) MUTANT WITH MET 13 REPLACED BY IRRD 3 ALPHA-AMINO-NORMAL-BUTYRIC ACID (M13ABA) IRRD 4 RIBONUCLEASE 4;	
1367	1mtf	A	31	130	3.4e-34	0.10	0.96		CHAIN: A, B;	HYDROLASE RNASE 4; HYDROLASE, RIBONUCLEASE, PHOSPHODIESTERASE
1367	1mtu		27	132	8.5e-45	-0.13	0.93		HYDROLASE/PHOSPHO RIC DIESTER RNA RIBONUCLEASE S (EC3.1.27.5) (PH 5.5) IRNU 3	
1367	1tra	A	28	132	1.7e-41	0.00	0.96		RIBONUCLEASE; CHAIN: A;	HYDROLASE RNASE A; HYDROLASE/PHOSPHORIC DIESTER, RIBONUCLEASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1367	1sm	A	27	114	1.7e-39	-0.20	0.90		HYDROLASE (NUCLEIC ACID/RNA)	
									SEMISYNTHETIC RIBONUCLEASE A (R*YNASE 1-118(COLOID))11-124) 1SRNA 3 (E.C.3.1.27.5) 1SRNA 1 1SRNA 2	
1388	1awq	A	42	193	1.7e-75			166.81	CYCLOPHILIN A; CHAIN: A; PEPTIDE FROM THE HIV-1 CAPSID PROTEIN; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) COMPLEX (ISOMERASE/PEPTIDE), CYCLOPHILIN A, HIV-1 CAPSID, 2 PSEUDO-SYMMETRY
1388	1cyt	A	39	194	3.4e-65			223.00	CYCLOPHILIN B; ICYN 6 CHAIN: A; ICYN 7 ID- (CHOLANTALALIB- CYCLOSPORIN; ICYN 10 CHAIN: G; ICYN 11	COMPLEX (ISOMERASE/PEPTIDE) ANT CYCLOSPORIN, ISOMERASE, ROTAMASE, SIGNAL ICYN 19
1392	1tal		28	112	0.0065	0.84	0.19		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1393	1f88	A	101	168	3.4e-06	-0.92	0.01		RHODOPSIN; CHAIN: A;	SIGNALING PROTEIN
									B	PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1423	1b6v	A	32	133	8.5e-49	0.31	1.00		RIBONUCLEASE; CHAIN: A; B;	MOLECULAR EVOLUTION, MOLECULAR EVOLUTION, RIBONUCLEASE
1423	1b6v	A	32	148	8.5e-49			77.74	RIBONUCLEASE; CHAIN: A; B;	MOLECULAR EVOLUTION, MOLECULAR EVOLUTION, RIBONUCLEASE
1423	1b6v	A	32	133	1e-47	0.01	0.87		HYDROLASE/PHOSPHO	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RIC DIESTER(RNA) RIBONUCLEASE (BOVINE, SEMINAL) (BS-RNASE) IRSR 3	
1423	1brt	A	32	148	1e-47			66.58	HYDROLASE/PHOSPHO RIBONUCLEASE (BOVINE, SEMINAL) (BS-RNASE) IRSR 3	
1423	1dy5	A	32	133	5.1e-47	0.38	1.00		RIBONUCLEASE A; CHAIN: A, B;	HYDROLASE (PHOSPHORIC DIESTER) RIBONUCLEASE, DEAMIDATION, ULTRA-HIGH RESOLUTION
1423	1qnt	A	30	133	3.4e-36	0.29	1.00		BOSINOPHIL CATIONIC PROTEIN; CHAIN: A;	RIBONUCLEASE RIBONUCLEASE 3, RNASE 3 BOSINOPHIL, RIBONUCLEASE, CYTOTOXICITY
1423	1rbd		46	133	8.5e-44	0.51	0.96		HYDROLASE/PHOSPHO RIBONUCLEASE 5 (EC3.1.27.5) MUTANT WITH MET 13 REPLACED BY IRBD 3 ALPHA-AMINO-NORMAL-BUTYRIC ACID (M13ABA) IRBD 4	
1423	1rbd		46	148	8.5e-44			77.31	HYDROLASE/PHOSPHO RIBONUCLEASE (RNA) RIBONUCLEASE 5 (EC3.1.27.5) MUTANT WITH MET 13 REPLACED BY IRBD 3 ALPHA-AMINO-NORMAL-BUTYRIC ACID (M13ABA) IRBD 4	
1423	1rnf	A	32	133	1.7e-35	0.36	0.95		HYDROLASE/PHOSPHO RIBONUCLEASE 4;	HYDROLASE RNASE 4;

Table 5

SEQ ID NO.	PDB ID	CHAIN N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1423	1rmf	A	33	152	1.7e-35			58.15	CHAIN: A, B; RIBONUCLEASE 4; CHAIN: A, B;	HYDROLASE, RIBONUCLEASE, PHOSPHODIESTERASE
1423	1rmu		32	133	3.4e-49	0.36	0.99		HYDROLASE/PHOSPHO RIC DIESTER.RNA RIBONUCLEASE S (E.C.3.1.27.5) (PH 5.5)	HYDROLASE, RIBONUCLEASE, PHOSPHODIESTERASE
1423	1rmu		32	148	3.4e-49			79.09	HYDROLASE/PHOSPHO RIC DIESTER.RNA RIBONUCLEASE S (E.C.3.1.27.5) (PH 5.5)	
1423	1rm	A	33	133	5.1e-45	0.04	0.99		RIBONUCLEASE, CHAIN: A; RIBONUCLEASE, CHAIN: A;	HYDROLASE RNASE A; HYDROLASE/PHOSPHO RIC DIESTER, RIBONUCLEASE
1423	1sm	A	32	133	3.4e-49	0.25	0.99		HYDROLASE (NUCLEIC ACID).RNA SEMISYNTHETIC RIBONUCLEASE A (R*NASE 1- 11)(COLON)11-124) ISR.N.3 (E.C.3.1.27.5) ISR.NA.1 ISR.NA.2	
1423	1sm	A	32	134	3.4e-49			80.10	HYDROLASE (NUCLEIC ACID).RNA SEMISYNTHETIC RIBONUCLEASE A (R*NASE 1- 11)(COLON)11-124) ISR.N.3 (E.C.3.1.27.5) ISR.NA.1 ISR.NA.2	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1427	1a4y	A	1	166	4e-20	0.16	-0.01		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (GL-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPIPTOP: MAPRNG, LEUCINE-RICH 3 REPEATS
1427	1a9n	A	1	129	6e-21	0.41	0.64		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>5</sub> ; CHAIN: A, C; U2 B <sub>5</sub> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SRRNP RIBONUCLEOPROTEIN
1427	1a9n	A	1	63	0.00017	0.07	0.63		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>5</sub> ; CHAIN: A, C; U2 B <sub>5</sub> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SRRNP RIBONUCLEOPROTEIN
1427	1a9n	A	33	179	4e-20	0.62	0.47		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>5</sub> ; CHAIN: A, C; U2 B <sub>5</sub> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SRRNP RIBONUCLEOPROTEIN
1427	1a9n	C	1	135	4e-21	0.40	0.37		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>5</sub> ; CHAIN: A, C; U2 B <sub>5</sub> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SRRNP RIBONUCLEOPROTEIN
1427	1a9n	C	33	179	8e-20	0.51	0.78		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A <sub>5</sub> ; CHAIN: A, C; U2 B <sub>5</sub> ; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA, RNA, SRRNP RIBONUCLEOPROTEIN
1427	1b1h	A	210	330	4e-10	0.44	0.11		HEMOGLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, I2PS-BINDING, HOMOPHILIC ADHESION
1427	1bpv		339	424	0.0015	-0.02	0.07		TTTR; CHAIN: NUL1;	CONNECTIN A71, CONNECTIN; TTTR; CONNECTIN, FIBRONECTIN TYPE III

Table 5

SEQ ID NO.	PDB ID	CHAIN N ID	STAR T AA	END AA	Pa Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1427	1e66	A	166	298	1.7e-10	-0.17	0.22		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1427	1e66	A	210	342	4e-13	0.27	0.24		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1427	1e95	C	229	360	1.4e-06	0.15	0.16		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1427	1e95	D	211	299	1e-16	0.50	0.62		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1427	1e95	D	229	350	5.1e-06	0.24	0.10		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1427	1d0b	A	1	154	3.4e-22	0.61	0.96		INTERMEDIATE B, CHAIN: A;	CELL ADHESION LECTINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1427	1d0c	A	1	115	4e-14	0.37	0.86		RAB GRIANVILGRIANVILTRA NSFERASE ALPHA SUBUNIT, CHAIN: A, C; RAB GRIANVILGRIANVILTRA NSFERASE BETA	TRANSFERASE CRYSTAL STRUCTURE, RAB GRIANVILGRIANVILTRA NSFERASE E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pa Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1427	1dec	A	20	135	8.5e-10	0.45	1.00		SUBUNIT; CHAIN: B, D; RAB GERANYLGERANYLTR NSPHERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTR NSPHERASE BETA SUBUNIT; CHAIN: B, D; OUTER ARM DYNEIN; CHAIN: A;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTR E 2.0 Å 2 RESOLUTION, N- FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1427	1d59	A	7	140	1.2e-18	0.22	0.65		CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA- BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	
1427	1e92	G	207	302	2e-17	0.57	0.37		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREPOIL FOLD
1427	1e92	G	222	342	2e-14	0.52	0.22		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREPOIL FOLD
1427	1e91	C	222	342	2e-14	0.34	0.35		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREPOIL FOLD
1427	1f9g	A	205	301	1.8e-18	0.38	0.59		TILKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL.



Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SFO/ROL D score	Compound	PDB annotation
1427	1fhh	A	154	422	4e-07			72.40	FIBRONECTIN: CHAIN: A <sub>1</sub>	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1427	1fhh	A	241	419	4e-07	0.37	0.33		FIBRONECTIN: CHAIN: A <sub>1</sub>	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1427	1fhh	A	318	416	6.8e-06	-0.42	0.43		FIBRONECTIN: CHAIN: A <sub>1</sub>	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1427	1fhh	A	340	442	0.00014	0.05	0.39		FIBRONECTIN: CHAIN: A <sub>1</sub>	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1427	1fhh	A	24	65	6.8e-05	-0.44	0.51		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B <sub>1</sub>	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP:RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1427	1fhh	A	2	62	1.7e-05	0.02	0.23		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B <sub>1</sub>	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP:RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1427	1fhh	B	24	65	6.8e-05	-0.49	0.43		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B <sub>1</sub>	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP:RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1427	1fhh	B	2	62	1.7e-05	0.15	0.76		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B <sub>1</sub>	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP:RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1427	1fhh	A	1	146	1.4e-11	0.09	-0.12		SGP2; CHAIN: A, C, B, G, L, K, M, Q, SRP1; CHAIN: B, D, F, H, J, L, N, P <sub>1</sub>	LIASE CYCLO-ACD32-ASSOCIATED PROTEIN 145; CYCLO-ACD32-ASSOCIATED PROTEIN P19; SGP1, SGP2, P-40X, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1427	1ts2	A	1	135	4e-16	0.17	-0.05		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D	PROTEIN LIGASE LIGASE CYCLIN A/CDC2-ASSOCIATED P45; CYCLIN A/CDC2-ASSOCIATED P19; SKP1, SKP2, P-BOX, LRR6, LUCIFIN- RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1427	1mth		333	419	2e-07	0.01	0.28		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1427	1mth		341	416	1e-06	-0.03	0.53		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1427	1mct		209	298	1e-19	0.43	0.92		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTIN; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1427	1mct	A	230	415	6e-06	0.34	-0.12		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1427	1ten		339	419	8e-07	-0.44	0.11		CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) (TEN 3	
1427	1mm		213	298	6e-18	0.64	0.65		MUSCLE PROTEIN TITIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pe Blast	Verity score	PMF score	SEQ/OL D score	Compound	PDB annotation
1427	1w6	A	211	364	2e-15	0.19	0.21		MODULE M5 (CONNECTIN) ITNM 3 (NMK MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	GLYCOPROTEIN CD4, IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MIC LIPOPROTEIN, POLYMORPHISM
1427	1wt		210	298	8e-19	0.50	0.31		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, 1 SET, MUSCLE
1427	1wnc	A	209	303	6e-21	0.20	0.15		NT-3 GROWTH FACTOR RECEPTOR TRKG; CHAIN: A;	TRANSPERASE TRK RECEPTOR, TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2
1427	1wv	X	215	302	1.4e-16	0.05	0.04		NERVE GROWTH FACTOR; CHAIN: V, W; TRKA RECEPTOR; CHAIN: X, Y;	NERVE GROWTH FACTOR/TRKA COMPLEX BETA-NF COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2 IMMUNOGLOBULIN LIKE DOMAIN, NERVE GROWTH
1427	1y8	A	2	166	1e-16	0.19	-0.09		GTPASE-ACTIVATING PROTEIN RNAL_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAP; RANGAP: GTPASE-ACTIVATING PROTEIN FOR SPL, GTPASE-ACTIVATING PROTEIN, GAP RNAP, RANGAP, TRK, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMISPHERAL TWINNING, 3 MERIODICAL TWINNING, MERIODICAL ACETYLATION RNASE
1427	20nh		1	170	4e-25	0.28	0.29		RIBONUCLEASE	

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T.AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									INHIBITOR; CHAIN: NULL;	INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1427	2nsh		2	323	1.7e-14	0.31	-0.07		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1427	2nsm		210	298	4e-16	0.29	0.70		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
1427	3nem	A	211	298	4e-18	0.52	0.48		NEURAL CELL ADHESION MOLECULE, LARGE ISOPHORA <sub>4</sub> CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1437	1dan	L	897	980	1.7e-11	0.01	-0.20		BLOOD COAGULATION FACTOR V1A; CHAIN: L <sub>1</sub> H <sub>1</sub> SOLUBLE TISSUE FACTOR; CHAIN: T, U, D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEINASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEINASE/COFACTOR/LIGAND)
1437	1dra	L	897	980	1.7e-11	0.06	-0.19		DES-GLA FACTOR V1A (B2AVY CHAIN); CHAIN: H, I, DES-GLA FACTOR	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

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Table 5

Seq ID NO:	PDB ID	CHAIN N/D	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1437	1dx5	1	703	808	5.1e-12	0.11	-0.20		VIIA (LIGHT CHAIN); CHAIN: L, M (DPN)-PEE-ARG-CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1437	1emm		652	729	5.1e-08	0.32	-0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCITONIN-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 BGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1437	1emm		703	767	6.8e-09	0.28	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCITONIN-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 BGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1437	1emm		817	884	3.4e-09	0.04	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCITONIN-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY,

Table 5

SIQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pa Blast	Verify score	PMF score	SIQ/FOL D score	Compound	PDB annotation
1437	1e6g	A	669	758	3.4e-08	0.20	-0.19		THERMAL HYSTERESIS PROTEIN ISOPFORM YL-1; CHAIN: A, B;	DISEASE MUTATION 3 BEG-LIKE DOMAIN HUMAN FIBRIN-1 FRAGMENT, MATRIX PROTEIN ANTIFREEZE PROTEIN INSECT ANTIFREEZE PROTEIN, THERMAL HYSTERESIS, TENERIO 2 MOLLUSC, IODINATION, RIGHT-HANDED BETA-HELIX, TMAP
1437	1hk	L	897	980	1.7e-11	0.16	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: L;	BLOOD CLOTTING COMPLEX/SERINE PROTEASE/COFACTOR/LIGAND, BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, BGF, COMPLEX (SERINE 4) PROTEASE/COFACTOR/LIGAND, BLOOD CLOTTING
1437	1k6		509	683	1.5e-08	0.18	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1437	1k6		580	735	1.7e-09	0.06	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1437	1k6		780	921	1.7e-13	0.02	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1437	1k6		824	989	3.4e-13	0.05	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1437	1k6		876	1056	3.4e-20	0.01	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1437	1pfx	L	523	618	5.1e-09	0.11	-0.20		FACTOR IXA; CHAIN: C; L; D-PHE-PRO-ARG; CHAIN: L;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR, COMPLEX, INHIBITOR, HEMOPHILIA/BGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1437	1qfk	L	901	980	8.5e-11	0.36	-0.17		COAGULATION FACTOR VIA (LIGHT CHAIN); CHAIN: L;	SERINE PROTEASE FVIIA, FVIIA; BLOOD COAGULATION, SERINE PROTEASE

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T.A.A	END A.A	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									COAGULATION FACTOR VIA (HEAVY CHAIN); INHIBITOR; CHAIN: C;	
1437	1ymo	A	570	741	4.4e-31	0.49	-0.12		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 YMO 3	
1437	1ymo	A	637	800	4.4e-26	0.78	-0.15		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 YMO 3	
1437	1ymo	A	687	878	1.3e-23	0.13	-0.18		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 YMO 3	
1437	1ymo	A	721	935	8.8e-22	0.23	-0.19		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 YMO 3	
1437	1ymo	A	819	985	6.6e-26	0.34	-0.19		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 YMO 3	
1437	1xka	L	777	861	1.7e-10	0.02	-0.20		BLOOD COAGULATION FACTOR XA; CHAIN: L; C;	BLOOD COAGULATION FACTOR; BLOOD COAGULATION FACTOR; SERINE PROTEINASE; EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1437	9wga	A	548	723	3.4e-12	0.27	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1437	9wga	A	601	775	8.5e-15	0.02	-0.19		LECTIN (AGGLUTININ)	

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	P4 Blast	Verity score	PMF score	SEQ/OL D score	Compound	PDB annotation
1437	9wga	A	647	816	8.5e-13	0.25	-0.19		WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
1437	9wga	A	734	918	1.7e-11	-0.00	-0.20		WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
1437	9wga	A	765	963	1.2e-14	0.13	-0.17		WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
1437	9wga	A	822	990	5.1e-13	0.05	-0.18		WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
1437	9wga	A	848	1016	5.1e-15	0.22	-0.17		WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
1442	144y	A	56	242	1.5e-15	0.11	0.28		WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
1442	144y	A	59	145	4.4e-09	-0.04	0.47		WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	
									WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA.3	



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Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pa Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
1442	1a9n	A	66	187	1.5e-22	0.46	1.00		CHAIN: B, D; U2 RNA HAIRPIN IV; CHAIN: Q, R, U2 A; CHAIN: A, C, U2 B*; CHAIN: B, D;	SNNP RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNNP RIBONUCLEOPROTEIN
1442	1a9n	C	59	158	6.6e-10	0.18	0.63		U2 RNA HAIRPIN IV; CHAIN: Q, R, U2 A; CHAIN: A, C, U2 B*; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNNP RIBONUCLEOPROTEIN
1442	1a9n	C	66	187	6.6e-22	0.17	0.98		U2 RNA HAIRPIN IV; CHAIN: Q, R, U2 A; CHAIN: A, C, U2 B*; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNNP RIBONUCLEOPROTEIN
1442	1a9n	C	89	200	1.8e-16	0.43	0.16		U2 RNA HAIRPIN IV; CHAIN: Q, R, U2 A; CHAIN: A, C, U2 B*; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNNP RIBONUCLEOPROTEIN
1442	1a0b	A	36	163	5.1e-21	0.67	1.00		INTERALIN B; CHAIN: A;	CELL ADHESION LIGAND RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1442	1a0b	A	39	186	8.8e-15	0.23	-0.07		INTERALIN B; CHAIN: A;	CELL ADHESION LIGAND RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1442	1a0c	A	38	140	3.4e-10	0.73	0.89		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT, CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT, CHAIN: B, D;	TRANSFERASE CRISTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE B, 2.0 A 2 RESOLUTION, N- FORMYL METHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1442	1a0c	A	57	163	6.8e-12	0.12	0.93		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT, CHAIN: B, D;	TRANSFERASE CRISTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE

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Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
									SUBUNIT, CHAIN: A, C; RAB GERANYLGERANYLTTRA NSPERASE BETA SUBUNIT, CHAIN: B, D; OUTER ARM DYNEIN; CHAIN: A;	E.2.0 A.2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1442	1ds9	A	47	162	1.7e-11	-0.02	0.84			CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA- BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1442	1lqv	A	35	162	6.8e-08	0.42	0.17		SKP2, CHAIN: A, C, E, G, I, K, M, O; SKP1, CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDC2- ASSOCIATED PROTEIN P45; CYCLIN A/CDC2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1442	1ls2	A	35	162	6.8e-08	0.23	0.22		SKP2, CHAIN: A, C; SKP1, CHAIN: B, D;	LIGASE CYCLIN A/CDC2- ASSOCIATED P45; CYCLIN A/CDC2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE- RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1442	1yrg	A	59	186	8.8e-14	-0.06	0.63		GTPASE-ACTIVATING PROTEIN RNAL, SCFPO, CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP, GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE- ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMISPHERAL TWINNING, 3 MEROPHERAL TWINNING, MICROHEDRY ACETYLATION INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR
1442	2bsh		56	266	1.3e-16	0.06	-0.05		RIBONUCLEASE INHIBITOR, CHAIN: NULL;	ACETYLATION INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PVR score	SEQ/OL D score	Compound	PDB annotation
1442	2bth		59	192	6.6e-20	-0.05	0.03		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1443	1aab		2	81	1e-27			73.20	HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1443	1aab		3	75	1e-27	0.34	1.00		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMG-BOX 1AAB 20
1443	1aab		83	123	1.5e-07	-0.51	0.17		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMG-BOX 1AAB 20
1443	1abt	A	5	75	6.8e-27	0.11	1.00		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-DY-Cp+CP+(DDO) CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA HMGI-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P36; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
1443	1abt	A	5	75	6.8e-27			65.26	HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-DY-Cp+CP+(DDO) CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA HMGI-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P36; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
1443	1tme		91	159	3.4e-10	-0.49	0.11		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Est Blast	Verify score	PMF score	SEQROL ID score	Compound	PDB annotation
1443	1b8m		91	163	5.1e-11	-0.42	0.42		(HMGB) (DNA-BINDING) IHME 3 HMGB-BOX DOMAIN B OF RAT HMGI) (NMR, 1 STRUCTURE) IHME 4	
1443	1b8m		91	163	5.1e-11	-0.42	0.42		DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMGI) BOX 2, COMPLEXED WITH IHSM 3	
1443	1b8m		91	163	5.1e-11	-0.42	0.42		MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) IHSM 4	
1443	1qrv	A	88	123	1.1e-08	-0.86	0.22		DNA (5'-Dp-Gp-Cp-Gp-Ap-Tp-Ap-Tp-Cp-Gp-Cp-3p); CHAIN: C, D, HIGH MOBILITY GROUP PROTEIN/D-CHAIN: A, B;	GENE REGULATION/DNA, HMGB-D-PROTEIN-DNA COMPLEX, HMGB DOMAIN, NON-SEQUENCE SPECIFIC 2 CHROMOSOMAL PROTEIN HMGB-D
1477	1mcy	C	232	316	1.4e-55	-0.63	0.06		DNA, CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1477	1ubd	C	214	316	9.8e-29	-0.76	0.16		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)
1482	1c9q	A	447	482	1.2e-06	-0.54	0.10		TRANSFORMING PROTEIN P21/H-RAS-1;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	P41 Bias	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1482	1dpc	A	400	482	6e-07	0.05	0.10		CHAIN: A; RHOD; CHAIN: A;	CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN GENE REGULATION/SIGNALING PROTEIN PROTEIN RHOD-GDP COMPLEX
1482	1huq	A	443	482	3.6e-07	-0.88	0.41		RAB5C; CHAIN: A;	PROTEIN TRANSPORT G- PROTEIN, GTP HYDROLYSIS, ENDOCYTOSIS, RAB PROTEIN, 2 MEMBRANE TRAFFICKING
1484	1buo	A	71	190	8.4e-16	-0.01	0.21		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	DOMAIN: PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION REVERSE TRANSCRIPTASE
1487	1nml		395	507	0.0018	-0.46	0.09		MAN1/ REVERSE TRANSCRIPTASE, 1NML 4 CHAIN: NULL; 1NML 5	
1489	1fex	A	104	403	0	0.67	1.00		BETA 1,4 GALACTOSYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE BETA4GALTI; NUCLEOTIDE BINDING PROTEIN, ALPHA BETA ALPHA FOLD
1489	1fex	A	94	404	0			343.91	BETA 1,4 GALACTOSYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE BETA4GALTI; NUCLEOTIDE BINDING PROTEIN, ALPHA BETA ALPHA FOLD
1491	1d1e	A	22	301	4.2e-10			61.55	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL, ALPHA-HELICAL, CONTRACTILE PROTEIN
1491	1d63	A	23	145	7e-31	-0.19	0.90		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE-BINDING PROTEIN 1; GMP, GTP HYDROLYSIS, GDP,

Table 5

SRQ ID NO:	PDB ID	CHAIN	STAR ID	END AA	Pa Blast	Verify score	PMF score	SEQPLOT D score	Compound	PDB annotation
1491	1b2a	A	23	145	7e-31	-0.39	0.92		INTERFERON-INDUCED GLYANILATE-BINDING PROTEIN I; CHAIN: A;	GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1491	1b2a	A	23	145	7e-31	-0.39	0.92		INTERFERON-INDUCED GLYANILATE-BINDING PROTEIN I; CHAIN: A;	SIGNALING PROTEIN GBP, GTP HYDROLYSIS GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, GMPBP, GPNBP.
1491	1b2i	P	25	273	7.2e-09	-0.34	0.01		NEUROLYSIN; CHAIN: P;	HYDROLASE NEUROPEPTIDASE, ZINC METALLOPEPTIDASE, ENDOPEPTIDASE
1493	1b2a	A	297	396	3.6e-07	-0.10	0.00		HYPOTHETICAL 23.7 KDA PROTEIN IN ICC-TOL C CHAIN: A, B;	HYDROLASE ADP-RIBOSE PYROPHOSPHATASE, NUDIX FOLD
1497	1b0w	A	1	95	7e-57			113.34	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES, IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
1497	1b0w	A	23	125	2.4e-63			123.78	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES, IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
1497	1b6d	A	23	124	5.6e-65	0.86	1.00		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
1497	1b1l	J	23	124	2.8e-66	0.85	1.00		FAB FRAGMENT; CHAIN: L, H, I, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12, VEGF COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
1497	1b0k	A	1	95	2.8e-56			113.70	HUYSIT; CHAIN: A, B, D, E, L1S027ME5; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MCRAMIDASE, HUMANIZED

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T.AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL ID score	Compound	PDB annotation
1497	1bvk	A	23	119	1.2e-63	0.95	1.00		HULYSH; CHAIN: A, B, D, E, LYSOZYME; CHAIN: C, F;	ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTI BODY/HYDROLASE)
1497	1bvk	A	23	125	1.2e-63			123.99	HULYSH; CHAIN: A, B, D, E, LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTI BODY/HYDROLASE) MURAMIDASE, HUMANIZED ANTI BODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTI BODY/HYDROLASE)
1497	1bw	A	21	125	2.8e-65			127.42	IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM
1497	1bw	A	23	124	2.8e-65	0.85	1.00		IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM
1497	1dee	A	23	124	7e-68	1.07	1.00		IGM RF 2A2; CHAIN: A, C, E, IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A;	IMMUNE SYSTEM F4B-1BP COMPLEX CRYSTAL STRUCTURE 2/7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPRANTIGEN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1497	1dql	L	1	95	5.6e-57			111.65	CHAIN: G, H; IGM MEZ IMMUNOGLOBULIN; CHAIN: L; IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	FAB VHS 3 SPECIFICITY IMMUNE SYSTEM IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
1497	1dql	L	23	125	7e-63			123.32	IGM MEZ IMMUNOGLOBULIN; CHAIN: L; IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
1497	1fgv	L	1	93	1.4e-60			121.32	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY H52 (HUH52-AA FV) IFGV 4	
1497	1fgv	L	23	124	4.2e-66	0.97	1.00		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY H52 (HUH52-AA FV) IFGV 4	
1497	1fgv	L	23	125	4.2e-66			131.86	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY H52 (HUH52-AA FV) IFGV 4	
1497	1fvc	A	1	95	1.1e-57			115.15	IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4DS, VERSION 8 IFVC3 IMMUNOGLOBULIN FV	
1497	1fvc	A	23	124	5.6e-64	0.82	1.00			



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pst Blast	Verify score	PME score	SEQ/OL D score	Compound	PDB annotation
									FRAGMENT OF HUMANIZED ANTIBODY 4DS, VERSION 8 1FVC.3	
1497	1Fvc	A	23	125	5.6e-64			125.91	IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4DS, VERSION 8 1FVC.3	
1497	1Fvd	A	23	124	2.8e-64	1.00	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4DS, VERSION 4 1FVD.3	
1497	1lgn	L	1	93	8.4e-59			113.29	IMMUNOGLOBULIN (IG-M) FV FRAGMENT 11GM.3	
1497	1lgn	L	23	124	4.2e-64	0.86	1.00		IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT 11GM.3	
1497	1lgn	L	23	125	4.2e-64			123.98	IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT 11GM.3	
1497	1wtl	A	1	93	4.2e-57			116.77	IMMUNOGLOBULIN WAT, A VARIABLE DOMAIN FROM IMMUNOGLOBULIN LIGHT-CHAIN 1WTL.3 (BENCE-JONES PROTEIN) 1WTL.4	
1497	1wtl	A	23	125	1.2e-63			127.46	IMMUNOGLOBULIN WAT, A VARIABLE DOMAIN FROM IMMUNOGLOBULIN	

Table 5

SEQ ID NO.	PDB ID	CHAIN N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQ/FOI, D score	Compound	PDB annotation
1497	2lgw	L	23	124	7e-67	0.94	1.00		LIGHT-CHAIN 1WTL3 (BENCE-JONES PROTEIN) 1WTL 4	
									IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTIBODY 2RGM 3 ANTIBODY H52 (H0H52-02 FAB) 2RGM 4	
1498	1a80		104	367	5.6e-69	0.12	0.99		2,5-DIKETO-D-GLUCONIC ACID REDUCTASE A; CHAIN: NULL;	OXIDOREDUCTASE 2,5-DKG REDUCTASE A; OXIDOREDUCTASE, ALPHA8BETA8 BARREL, 2,5-DIKETO-D-GLUCONIC 2 ACID, COMMERCIAL VITAMIN C SYNTHESIS
1498	1a80		122	372	5.6e-69			62.58	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE A; CHAIN: NULL;	OXIDOREDUCTASE 2,5-DKG REDUCTASE A; OXIDOREDUCTASE, ALPHA8BETA8 BARREL, 2,5-DIKETO-D-GLUCONIC 2 ACID, COMMERCIAL VITAMIN C SYNTHESIS
1498	1ads		105	365	2.8e-84	0.05	0.96		OXIDOREDUCTASE ALDOSE REDUCTASE (EC.1.1.1.21) COMPLEX WITH NADPH 1ADS 3	
1498	1ads		82	372	2.8e-84			105.14	OXIDOREDUCTASE ALDOSE REDUCTASE (EC.1.1.1.21) COMPLEX WITH NADPH 1ADS 3	
1498	1afs	A	68	372	1.1e-72			101.13	3-ALPHA-HYDROXYSTEROID DIHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE 3-ALPHA-HSD; OXIDOREDUCTASE, NAD

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Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Pos Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1498	1ab5	A	99	368	1.1e-72	0.16	0.83		3-ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE 3-ALPHA-HSD, OXIDOREDUCTASE, NAD
1498	1ab4		105	365	1.1e-83	-0.09	0.94		ALDOSE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE, ALDOSE REDUCTASE, INHIBITION, DIABETES
1498	1ab4		81	372	1.1e-83			103.47	ALDOSE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE, ALDOSE REDUCTASE, INHIBITION, DIABETES
1498	1c9w	A	105	365	2.8e-81	0.12	0.84		CHO REDUCTASE; CHAIN: A;	OXIDOREDUCTASE, ALPHA/BETA TIM BARREL, PROTEIN-NADP+ COMPLEX
1498	1c9w	A	80	372	2.8e-81			103.01	CHO REDUCTASE; CHAIN: A;	OXIDOREDUCTASE, ALPHA/BETA TIM BARREL, PROTEIN-NADP+ COMPLEX
1498	1cwn		106	368	9.8e-78	0.09	0.70		ALDEHYDE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE ALR1, TIM-BARREL, OXIDOREDUCTASE, NADP
1498	1cwn		79	372	9.8e-78			81.73	ALDEHYDE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE ALR1, TIM-BARREL, OXIDOREDUCTASE, NADP
1498	1cl3	A	102	365	2.8e-85	0.21	0.99		ALDOSE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE, ALDOSE REDUCTASE, INHIBITION, DIABETES
1498	1cl3	A	82	372	2.8e-85			106.54	ALDOSE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE, ALDOSE REDUCTASE, INHIBITION, DIABETES
1498	1tfb		105	365	1.4e-80	0.08	0.90		FR-1 PROTEIN; CHAIN: NULL;	OXIDOREDUCTASE (NADP) ALDO-KETO OXIDOREDUCTASE (NADP), TIM BARREL, OXIDOREDUCTASE (NADP)
1498	1tfb		80	372	1.4e-80			98.60	FR-1 PROTEIN; CHAIN: NULL;	OXIDOREDUCTASE (NADP)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pa Blast	Verify score	PMF score	SEQPROL D score	Compound	PDB annotation
									NULL;	ALDO-KETO OXIDOREDUCTASE (NADP), TIM BARREL
1498	1hw6	A	104	367	1.4e-66	0.15	0.90		2,5-DIKETO-D-GLUCONIC ACID REDUCTASE, CHAIN: A;	OXIDOREDUCTASE AFO-2,5-DIKETO-D-GLUCONATE REDUCTASE, TIM BARREL
1498	1hw6	A	113	365	1.4e-66			67.97	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE, CHAIN: A;	OXIDOREDUCTASE AFO-2,5-DIKETO-D-GLUCONATE REDUCTASE, TIM BARREL
1498	2air		106	368	1.1e-76	0.22	0.70		ALDEHYDE REDUCTASE, CHAIN: NULL;	OXIDOREDUCTASE ALR1; OXIDOREDUCTASE, TIM-BARREL
1498	2air		79	372	1.1e-76			61.33	ALDEHYDE REDUCTASE, CHAIN: NULL;	OXIDOREDUCTASE ALR1; OXIDOREDUCTASE, TIM-BARREL
1499	1ftm	A	543	626	1.2e-18	0.33	-0.18		OUTER SURFACE PROTEIN C; CHAIN: A, B, C, D;	IMAGINE SYSTEM OSRC, LYME DISEASE, OSRC, HB19, HELICAL BUNDLE, DIMER
1499	1ftm	A	550	626	3.6e-17	0.14	-0.15		OUTER SURFACE PROTEIN C; CHAIN: A, B, C, D;	IMAGINE SYSTEM OSRC, LYME DISEASE, OSRC, HB19, HELICAL BUNDLE, DIMER
1499	1ftm	A	551	626	9.6e-17	0.32	-0.20		OUTER SURFACE PROTEIN C; CHAIN: A, B, C, D;	IMAGINE SYSTEM OSRC, LYME DISEASE, OSRC, HB19, HELICAL BUNDLE, DIMER
1499	1g5z	A	550	626	1.2e-17	0.36	-0.19		OUTER SURFACE PROTEIN C; CHAIN: A;	IMAGINE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1499	1g5z	A	550	626	3.6e-17	0.04	-0.20		OUTER SURFACE PROTEIN C; CHAIN: A;	IMAGINE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1499	1g5z	A	551	626	1.2e-17	0.34	-0.19		OUTER SURFACE PROTEIN C; CHAIN: A;	IMAGINE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1499	1g5z	A	551	626	1.2e-17	0.32	-0.20		OUTER SURFACE PROTEIN C; CHAIN: A;	IMAGINE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1499	1g5z	A	551	626	2.4e-17	0.18	-0.19		OUTER SURFACE	IMAGINE SYSTEM SURFACE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pa Blast	Verify score	PMF score	SIQPOL D score	Compound	PDB annotation
1499	1g5c	A	551	626	3.6e-17	0.67	-0.19		PROTEIN C; CHAIN: A; OUTER SURFACE PROTEIN C; CHAIN: A; CD46; CHAIN: A, B, C, D, E, F;	PROTEIN, ALPHA HELIX PROTEIN IMMUNE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
1504	1gd	A	10	79	1.4e-30			90.17	CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
1504	1gd	A	1	72	2.8e-24			89.35	CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
1504	1gd	A	222	347	1.4e-27			222.13	CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
1504	1gd	A	77	344	7e-35			81.51	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
1504	1g44	A	166	406	5.6e-31			69.90	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1504	1g44	B	220	406	1.4e-25			74.78	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1504	1g44	C	153	406	5.6e-24			69.94	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1504	1g4b	A	74	406	4.2e-28			74.76	HUMAN BETA-2-	MEMBRANE ADHESION SHORT

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMR score	SEQPOL D score	Compound	PDB annotation
									GLYCOPROTEIN I, CHAIN: A;	CONSENSUS REPEAT SUSHI, COMPLEMENT CONTROL PROTEIN, 2-N-GLYCOSYLATION, MUTU-DOMAIN, MEMBRANE ADHESION
1511	1alh	A	281	363	4.2e-29	-0.50	0.03		QGRS ZINC FINGER PEPTIDE, CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1511	1alh	A	367	436	2.8e-26	-0.33	0.28		QGRS ZINC FINGER PEPTIDE, CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1511	1bbo		369	424	4.2e-14	-0.42	0.42		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 111BB0 3 REPLACED BY ABBU (C11ABU) (NMR, 60 STRUCTURES) 1BB0 4	
1511	1mey	C	10	73	1.4e-40			64.91	DNA, CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	1mey	C	280	363	2.8e-47	-0.07	0.39		DNA, CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	1mey	C	309	391	2.8e-49	-0.12	1.00		DNA, CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA)

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Table 5

SFQ ID No.	PDB ID	CHAIN ID	STAR T AA	END AA	Peptide Blast	Verify score	PMF score	SFQROL D score	Compound	PDB annotation
1511	Imey	C	338	421	286-49	0.17	1.00		CONSENSUS ZINC FINGER, PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	Imey	C	338	421	286-49	0.17	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER, PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	Imey	C	338	424	286-49			63.28	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER, PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	Imey	C	366	437	286-40	-0.25	0.15		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER, PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	Imey	G	336	363	566-13	0.73	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER, PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	Imey	A	235	400	146-35	-0.57	0.33		THILA; CHAIN: A, D, SS; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2
1511	Imey	A	279	449	146-35			65.99	THILA; CHAIN: A, D, SS; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TRANSCRIPTION INITIATION, ZINC FINGER, PROTEIN
1511	Imey	A	279	449	146-35			65.99	THILA; CHAIN: A, D, SS; RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1511	1ubd	A	339	447	4,2e-24	-0.51	0.06		TFIIIA, CHAIN: A, D, SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
									COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	
1511	1ubd	C	309	420	6e-35			68.77	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
									YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1511	1ubd	C	314	419	1.4e-34	-0.02	0.87		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
									YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1511	1ubd	C	324	403	6e-35	-0.34	0.37		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
									YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1511	1ubd	C	346	436	4.2e-28	-0.08	0.15		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION



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Table 5

Seq ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SeqPOL D score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B.	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1511	2gi1	A	288	421	2.8e-33	-0.30	0.22		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; GIL1, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1511	2gi1	A	309	449	2.8e-33			63.97	ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; GIL1, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1511	2gi1	A	317	435	7e-31	0.05	0.77		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; GIL1, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1511	2gi1	A	346	446	1.1e-22	0.09	-0.15		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; GIL1, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1513	1hi7	A	139	173	0.0015	-0.26	0.06		PS2 PROTEIN; CHAIN: A, B;	GROWTH FACTOR PVR-2, PS2, TFF1, BREAST CANCER ESTROGEN INDUCIBLE GROWTH FACTOR, CELL MOTILITY, TUMOR SUPPRESSOR, TREFOL 2 DOMAIN, SIGNAL
1518	1bm6		21	116	1.4e-34			131.75	BETA-2-MICROGLOBULIN; 1BM6 5 CHAIN: NULL 1BM6 6	HISTOCOMPATIBILITY ANTIGEN IACTOLIN, MHC-1 HISTOCOMPATIBILITY ANTIGEN, LIGHT CHAIN 1BM6 11
1518	14af	B	1	85	7e-31			134.89	HLA CLASS I	IMMUNE SYSTEM MAGE-4

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	P4 Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1518	1i4f	B	20	116	2.8e-34			157.82	HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN; A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C	ANTIGEN, MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1521	1bnp		12	115	4.2e-49			156.36	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN; A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C	IMMUNE SYSTEM MAGE-4 ANTIGEN, MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1521	1bnp		638	741	4.2e-50	0.56	1.00		BONE MORPHOGENETIC PROTEIN-7; CHAIN: N1LL;2	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
1521	1bnp		638	741	4.2e-50	0.56	1.00		BONE MORPHOGENETIC PROTEIN-7; CHAIN: N1LL;2	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
1521	1bnp		638	741	4.2e-50			156.52	BONE MORPHOGENETIC PROTEIN-7; CHAIN: N1LL;2	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
1521	1poc	A	40	257	7e-39	0.29	0.62		GLUTAMONATE COBENZYLME A-	TRANSFERRIN TRANSFERASE, COB, GLUTAMATE, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMR score	SEQPOL ID score	Compound	PDB annotation
1521	1poi	A	53	244	1.1e-51	0.22	0.21		TRANSFERASE; CHAIN: A, B, C, D;	FERMENTATION
1521	1poi	A	53	244	1.1e-51	0.22	0.21		GLUTACONATE COENZYME A- TRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE TRANSFERASE, COA, GLUTAMATE, PROTEIN FERMENTATION
1521	1poi	B	270	490	3.6e-60	0.13	0.93		GLUTACONATE COENZYME A- TRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE TRANSFERASE, COA, GLUTAMATE, PROTEIN FERMENTATION
1521	1poi	B	273	501	2.8e-34	0.01	0.83		GLUTACONATE COENZYME A- TRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE TRANSFERASE, COA, GLUTAMATE, PROTEIN FERMENTATION
1523	1atl	A	221	422	4.2e-39	0.70	1.00		ATROLYSIN C; IATL 4 CHAIN: A, B, C, D; IATL 5	METALLOENDOPEPTIDASE HEMORRHAGIC TOXIN C, FORM D, IATL 6
1523	1atl	A	223	422	1.2e-42	0.73	1.00		ATROLYSIN C; IATL 4 CHAIN: A, B, C, D; IATL 5	METALLOENDOPEPTIDASE HEMORRHAGIC TOXIN C, FORM D, IATL 6
1523	1bkc	A	222	421	1.2e-43	-0.25	0.17		TUMOR NECROSIS FACTOR-ALPHA- CONVERTING ENZYME; CHAIN: A, C, E, I;	ZN-ENDOPEPTIDASE TACE; ZN-ENDOPEPTIDASE, HYDROLASE, TNF-ALPHA
1523	1bkc	A	225	417	9.8e-07	0.03	0.01		TUMOR NECROSIS FACTOR-ALPHA- CONVERTING ENZYME; CHAIN: A, C, E, I;	ZN-ENDOPEPTIDASE TACE; ZN-ENDOPEPTIDASE, HYDROLASE, TNF-ALPHA
1523	1bnd	A	222	420	2.8e-36	0.65	0.87		ACUTOLYSIN A; CHAIN: A;	TOXIN HEMORRHAGIC I, IAH-I; METALLOPROTEINASE, SNAKE VENOM, MMR, TOXIN
1523	1dm	L	662	718	1.4e-07	0.34	0.23		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H <sub>2</sub> SOLUBLE TISSUE	BLOOD COAGULATION, SERINE PROTEINASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMR score	SID/PROL D score	Compound	PDB annotation
1523	1dva	L	662	718	1.4e-07	0.53	0.18		FACTOR: CHAIN: T, U, D, PHE-PHE-ARG-CHLOROETHYLKETONE (DEFRICK) WITH CHAIN: C	INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR(LIGAND))
1523	1dva	L	662	718	1.4e-07	0.53	0.18		DES-GLA FACTOR VIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN+PEPTIDE COMPLEX
1523	1emm		589	656	2.8e-11	0.15	-0.17		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1523	1emm		629	690	1.4e-09	0.19	0.06		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1523	1emm		663	718	4.2e-07	0.40	-0.01		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast score	Verify score	PMR score	SEQPOL ID score	Compound	PDB annotation
1523	1ak	L	662	718	1.4e-07	0.64	0.25		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; SL15; CHAIN: I;	DOMAIN: HUMAN FIBRIN(LIN-1) FRAGMENT; MATRIX PROTEIN BLOOD CLOTTING COMPLEXSERINE PROTEASE/COFACTOR(LGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4) PROTEASE/COFACTOR(LGAND), BLOOD CLOTTING
1523	1ei		439	508	4.2e-15	-0.04	0.84		FLAVORIDIN; 1EVL 4 CHAIN: NUTL 1EVL 5	BLOOD COAGULATION INHIBITOR GP IIB/IIIA ANTAGONIST 1EVL 9
1523	1ei		439	512	1.2e-26	0.36	0.94		FLAVORIDIN; 1EVL 4 CHAIN: NUTL 1EVL 5	BLOOD COAGULATION INHIBITOR GP IIB/IIIA ANTAGONIST 1EVL 9
1523	1iag		221	422	2.8e-38	0.77	1.00		METALLOPROTEINASE ADAMALYSIN II (PROTEINASE II) (E.C.3.4.24.46) 1IAG 3	
1523	1iag		223	422	4.8e-41	0.65	1.00		METALLOPROTEINASE ADAMALYSIN II (PROTEINASE II) (E.C.3.4.24.46) 1IAG 3	
1523	1igr	A	410	706	1.2e-11	0.15	-0.19		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
1523	1ko		461	630	7e-20	0.09	-0.13		LAMININ; CHAIN: NUTL; CHAIN: A;	GLYCOPROTEIN GLYCOPROTEIN
1523	1ko		519	664	2.8e-11	0.22	-0.17		LAMININ; CHAIN: NUTL; CHAIN: A;	GLYCOPROTEIN GLYCOPROTEIN
1523	1ko		638	774	1.4e-10	0.07	-0.20		LAMININ; CHAIN: NUTL; CHAIN: A;	GLYCOPROTEIN GLYCOPROTEIN
1523	1kar		439	508	1.3e-15	0.18	0.35		AGGREGATION INHIBITOR, GP	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMR score	SEQPOL ID score	Compound	PDB annotation
1523	1kst		439	510	3.6e-25	0.31	0.60		ANTAGONIST KISTRIN (NMNR, 8 STRUCTURES) KIST 3	
1523	1pfx	L	662	718	9.8e-08	0.53	0.72		FACTOR IXA; CHAIN: C <sub>1</sub> ; D-PHE-PRO-ARG; CHAIN: I; KIST 3	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR, COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1523	1qua	A	221	420	3.6e-39	0.63	1.00		ACUTOLYSIN-C; CHAIN: A;	TOXIN HEMORRHAGIN III METALLOPROTEASE, HEMORRHAGIC TOXIN, SNAKE VENOM PROTEINASE, 2 CRYSTAL STRUCTURE, AGKISTRONON ACUTUS
1523	1qua	A	221	420	9.8e-35	0.82	1.00		ACUTOLYSIN-C; CHAIN: A;	TOXIN HEMORRHAGIN III METALLOPROTEASE, HEMORRHAGIC TOXIN, SNAKE VENOM PROTEINASE, 2 CRYSTAL STRUCTURE, AGKISTRONON ACUTUS
1523	1qub	A	414	693	1.2e-11	0.01	-0.17		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT SLIHL, COMPLEMENT CONTROL, PROTEIN 2 N-GLYCOSYLATION, MULTIDOMAIN, MEMBRANE ADHESION
1523	2sch		469	516	2.4e-18	-0.19	0.30		BLOOD COAGULATION	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Bias	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									INHIBITOR ECHISTATIN (NMN, 8 STRUCTURES) ZECH 3	
1523	9wga	A	502	666	2.8e-16	0.27	0.65		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1523	9wga	A	526	701	1.4e-12	0.09	0.23		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1523	9wga	A	661	859	7e-15	0.08	-0.14		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1524	1alh	A	21	103	5.6e-31			75.55	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OF OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1524	1alh	A	2	84	4.2e-31			77.96	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OF OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1524	1alh	A	58	140	4.2e-31			77.62	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OF OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1524	1alh	A						104.44	ATRIOLYSIN G, IATL 4	METALLOENDOPETIDASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	1st Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1524	1bnd	A	10	208	5.6e-71			97.67	CHAIN: A, B, C, D; 1A1L 5 ACTUOLYSIN A; CHAIN: A;	HEMORRHAGIC TOXIN C <sub>1</sub> FORM D; 1A1L 6 TOXIN HEMORRHAGIC 1, 1A1H-4; METALLOPROTEINASE, SNAKE VENOM, AMP, TOXIN
1524	1cfe		30	184	4.2e-42			82.74	PATHOGENESIS-RELATED PROTEIN P144; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN P144; CHAIN: NULL; ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1
1524	1w1		13	88	1.4e-25			67.46	FLAVORIDIN; 1PVL 4 CHAIN: NULL, 1PVL 5	BLOOD COAGULATION INHIBITOR GP IIB/IIIA ANTAGONIST 1PVL 9
1524	1lag		7	210	4.2e-74			105.32	METALLOPROTEINASE ADAMALYSIN II (PROTEINASE II) (E.C.3.4.24.46) 1LAG 3	
1524	1jln	A	21	247	2.8e-45	-0.00	-0.09		PROTEIN TYROSINE PHOSPHATASE RECEPTOR TYPE R; CHAIN: A;	HYDROLASE STELLATE PTASE; PROTEIN-TYROSINE-PTASE PHOSPHATASE, PTP-SL, PTPBR; ERK2-MAP 2 KINASE REGULATION
1524	1lkt		13	85	4.2e-25			66.02	AGGREGATION INHIBITOR, GP ANTAGONIST KISTRIN (NMR, 8 STRUCTURES) 1KST 3	
1524	1mcy	C	1	64	2.8e-38			60.19	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pa Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1524	Imey	C	1	66	1.1e-39			68.19	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1524	Imey	C	29	111	4.2e-50			93.01	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1524	Imey	C	48	130	2.8e-50			95.82	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1524	Imey	C	57	139	1.4e-50			95.58	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1524	Imey	C	57	139	2.8e-50			95.19	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1524	Imkp							132.82	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
1524	Imkp		9	151	2.8e-34			133.40	PYSTI; CHAIN: NULL;	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
1524	Imnx	A	1	187	4.2e-44			81.43	VES V 5; CHAIN: A;	ALLBROEN ANTIGEN 5; ANTIGEN 5, ALLBROEN, VESPH VIBROM TOXIN HEMORRHAGIN III
1524	Imux	A	7	208	7e-69			109.26	ACUTOLYSIN-C; CHAIN:	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMR score	SEQ/OL D score	Compound	PDB annotation
1524	1t6m	A	18	241	2.8e-59	0.04	0.35		RECEPTOR PROTEIN TYROSINE PHOSPHATASE M0; CHAIN: A, B	RECEPTOR D1, RECEPTOR PHOSPHATASE, SIGNAL TRANSDUCTION, ADHESION, 2 HYDROLASE
1524	1t66	A	1	153	4.2e-37			71.61	TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1524	1t66	A	1	153	5.6e-37			107.29	TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1524	1t66	A	1	153	7e-38			101.40	TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1524	1t66	A	3	144	8.4e-34			66.54	TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) RNA POLYMERASE III, 2

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1524	1ubd	C	1	111	4.2e-36			84.52	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	TRANSCRIPTION INITIATION, ZINC FINGER, PROTEIN
1524	1ubd	C	20	130	5.6e-36			88.82	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1524	1ubd	C	31	139	2.8e-36			88.27	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1524	1ubd	C	3	111	1.4e-35			83.28	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1524	1vhr	A	81	250	2.4e-34			87.98	HUMAN VHL-RELATED	HYDROLASE VHR; HYDROLASE,

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Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR TAA	END AA	Pd Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1524	1htc	A	88	249	2.4e-34	0.36	1.00		DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B	PROTEIN DUAL-SPECIFICITY PHOSPHATASE
1524	2gfi	A	1	131	7e-33			76.01	HUMAN VH1-RELATED DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B	HYDROLASE VHR. HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE
1524	2gfi	A	1	140	2.8e-33			83.07	ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1524	2gfi	A	1	140	2.8e-33			88.13	ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1524	2gfi	A	1	140	7e-34			91.46	ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIL1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1527	1das	A	321	387	0.0056	0.18	0.34		M0882; CHAIN: A;	STRUCTURAL GLOBULINS, HYPOTHETICAL PROTEIN, METIANOCOCUS JANNASCHII
1527	1d6q	1	293	382	0.00048	0.14	0.18		HNRNP ARGININE N-DOMAIN, BETA-BARREL, MIXED CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERRASE SAAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1528	1q4		52	207	5.6e-43	-0.34	0.15		TROPONIN C; CHAIN: NDL1;	MUSCLE PROTEIN CTRC, CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1528	1aui	B	245	399	1.3e-34	-0.11	0.00		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A-B	HYDROLASE CALCIUM-INTRIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1528	1edm	A	251	391	4.2e-53	-0.23	0.29		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
1528	1edm	A	324	415	4.2e-28	-0.18	0.11		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
1528	1ell		251	391	5.6e-58	-0.39	0.40		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICCL 3	
1528	1ell		324	415	7e-29	0.03	0.11		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICCL 3	
1528	1entf		322	391	1.4e-30	-0.09	0.59		CALMODULIN (VERTEBRATE); ICMF 6	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE); ICMF 6
1528	1del	A	52	207	1.1e-39	-0.09	0.23		CHAIN: NITILE; ICMF 7	CALMODULIN APO TRIC- DOMAIN; ICMF 9
1528	1ext	A	249	390	5.6e-56	0.10	0.05		CARDIAC TROPONIN C; CHAIN: A	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1528	1ext	A	320	415	9.8e-28	-0.09	0.16		CALMODULIN; CHAIN: A <sub>1</sub>	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER METAL TRANSPORT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PAM score	SEQPOL D score	Compound	PDB annotation
1528	1hw4	A	255	310	2.8e-15	0.09	-0.12		A <sub>1</sub>	CALMODULIN, HIGH RESOLUTION, DISORDER
									A <sub>2</sub>	METAL BINDING PROTEIN EF-HAND, HELIX-LOOP-HELIX, FRAGMENT, CALCIUM, TR2C, C-2
										TERMINAL DOMAIN, CALMODULIN
1528	1hw4	A	327	390	9.8e-30	0.25	0.65		CALMODULIN; CHAIN: A <sub>2</sub>	METAL BINDING PROTEIN EF-HAND, HELIX-LOOP-HELIX, FRAGMENT, CALCIUM, TR2C, C-2
										TERMINAL DOMAIN, CALMODULIN
1528	1g8i	A	234	386	2.8e-26	-0.23	0.07		NEURONAL CALCIUM SENSOR 1; CHAIN: A, B, C	METAL BINDING PROTEIN FREQUENTIN; CALCIUM BINDING-PROTEIN, EF-HAND, CALCIUM ION
1528	1j10	A	63	203	7e-17	-0.56	0.65		OBEILIN; CHAIN: A <sub>2</sub>	LUMINESCENT PROTEIN BIOLUMINESCENCE, CALCIUM-REGULATED PHOTOPROTEIN, OBEILIN, 2 OBEILIN, HYDROID
1528	1j12	A	63	203	1.1e-16	-0.09	0.12		OBEILIN; CHAIN: A <sub>2</sub>	LUMINESCENT PROTEIN BIOLUMINESCENCE, CALCIUM-REGULATED PHOTOPROTEIN, OBEILIN, 2 OBEILIN, HYDROID
1528	1icf		245	391	4.2e-46	-0.14	0.51		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION, MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, P-F HAND, 2 OPEN CONFORMATION, REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1528	1inx		251	390	4.2e-43	0.04	0.10		TROPONIN C; TTNX 4 CHAIN: NULL; TTNX 5	CALCIUM-BINDING PROTEIN EF-HAND TTNX 14

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1528	1tux		324	415	9.8e-26	-0.22	0.07		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5 CONTRACTIONS SYSTEM C	CALCULIN-BINDING PROTEIN EF-HAND ITNX 14
1528	1top		251	393	9.8e-47	-0.07	0.11		CONTRACTILE SYSTEM C	
1528	1top		324	415	9.8e-26	-0.41	0.15		CONTRACTILE SYSTEM C	
1528	1vfk	A	249	390	2.8e-56	-0.01	0.22		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX/CALCIUM-BINDING PROTEIN/PEPTIDE
1529	1dbs	A	153	449	4.2e-61	-0.31	0.05		GDP-MANNANOSE 4,6-DEHYDRATASE; CHAIN: A;	LYASE DEHYDRATASE, NADP, GDP-MANNANOSE, GDP-FUCOSE
1533	1a17		39	185	2.8e-13	0.07	-0.08		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE
1533	1a17		419	532	1.4e-18	0.48	0.12		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	TETRA/TRICOPEPTIDE, TRP- HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1533	1a17		9	134	4.2e-16	0.14	-0.12		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE
										TETRA/TRICOPEPTIDE, TRP- HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pa Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1533	1e1r	A	184	284	1.1e-14	0.21	-0.02		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1533	1e1r	A	414	505	4.2e-15	0.34	0.25		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1533	1e1r	A	450	540	1.4e-13	0.36	0.30		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1533	1e1r	A	45	144	5.6e-11	0.14	0.06		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1533	1e1w	A	184	300	7e-17	0.17	0.46		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1533	1e1w	A	423	524	4.2e-15	0.55	0.58		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1533	1e1w	A	42	154	9.8e-10	0.20	-0.17		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1533	1e1w	A	451	558	4.2e-15	0.58	0.07		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1533	1e1w	A	484	591	1.4e-15	0.02	-0.19		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pa Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1533	1dhw	A	9	120	2.8e-15	0.18	-0.14		PEPTIDE; CHAIN: C, D;	REPEAT, HSC70 2 HSP70, PROTEIN BINDING
1533	1dht	A	219	532	3.6e-11	0.14	0.58		TPR1-DOMAIN OF HOX-PEPTIDE COMPLEX, HELICAL PEPTIDE; CHAIN: C, D;	CHAPERONE HOX-TPR1-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70 2 HSP70, PROTEIN BINDING
1533	1dht	A	319	598	1.3e-30	-0.00	-0.15		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTSI-1BP, PEROXIN-5, PTSI PROTEIN-PEPTIDE COMPLEX, TETRA-TRICOPEPTIDE REPEAT, TPR 2 HELICAL REPEAT
1533	1dht	A	10	140	7e-12	0.04	-0.12		NEUTROPHIL CYTOSOL FACTOR 2; CHAIN: A;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTSI-1BP, PEROXIN-5, PTSI PROTEIN-PEPTIDE COMPLEX, TETRA-TRICOPEPTIDE REPEAT, TPR 2 HELICAL REPEAT
1533	1dht	A	451	539	2.8e-08	0.20	-0.11		PEROXISOME TARGETING SIGNAL 1 RECEPTOR PEPS;	PHAGOCYTE OXIDASE FACTOR P67Hox, NCF-2; PHAGOCYTE OXIDASE FACTOR, SH3 DOMAIN, REPEAT, TPR REPEAT
1533	1dht	A	409	538	9.8e-14	0.29	-0.08		PEROXISOME TARGETING SIGNAL 1 RECEPTOR PEPS;	TRANSPORT PROTEIN PEPS; ALPHA HELICAL
1533	1dht	A	444	519	7.2e-07	0.04	0.63		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PHASE MINUNOPHILIN TETRA-TRICOPEPTIDE
1533	1dht	A	444	519	7.2e-07	0.04	0.63		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PHASE MINUNOPHILIN TETRA-TRICOPEPTIDE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SIQ/OL D score	Compound	PDB annotation
1533	1hg	A	449	572	1.4e-12	0.15	-0.14		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPIASE IMMUNOPHILIN TETRAPEPTIDE
1533	1hg	A	483	586	5.6e-11	0.17	-0.19		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPIASE IMMUNOPHILIN
1534	1b07	A	635	667	0.0084	-0.19	0.03		PROTO-ONCOGENE CRK (CRK); CHAIN: A; HIS TAG; CHAIN: B; SH3 PEPTOID INHIBITOR; CHAIN: C;	SH3 DOMAIN 198; ADAPTER MOLECULE CRK; SH3 DOMAIN; INHIBITORS, PEPTOIDS, PROTEIN-PROTEIN 2 RECOGNITION, PROLINE-RICH MOTIFS, SIGNAL TRANSDUCTION
1534	1b0x	A	692	753	3.6e-12	0.84	1.00		EPH4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE; PROTEIN INTERACTION MODULE 2 DIMERIZATION DOMAIN; TRANSFERASE
1534	1br	A	635	674	0.00024	-0.01	0.06		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL IGBR, 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE IGBR 4 (NMR, 29 STRUCTURES) IGBR 5	
1534	1brq	B	635	670	2.4e-06	0.13	0.00		GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; CHAIN: A, B, YAV/PROTO ONCOGENE; CHAIN: C;	SIGNALING PROTEIN/SIGNALING PROTEIN SH3 DOMAIN; PROTEIN-PROTEIN COMPLEX, GRB2, YAV

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	P4 Bias	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1534	1hsq		635	675	0.00096	-0.39	0.10		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C- GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) IHSO 3 (NMR, MINIMIZED MEAN STRUCTURE) IHSO 4	
1534	1pwt		635	670	0.00024	-0.05	0.07		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1534	1sem	A	635	667	7.2e-06	-0.15	0.07		SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D ISEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, ISEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR ISEM 19
1534	1seg		692	753	1.2e-11	0.53	0.94		EPHRIIN TYPE-B RECEPTOR 2; CHAIN: NULL;	TYROSINE-PROTEIN KINASE NMR RECEPTOR OLIGOMERIZATION EPH RECEPTOR; TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE
1534	1uc		635	676	3.6e-06	-0.55	0.13		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPRING PROTEIN, CALCINE-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1538	1a06		1	270	1.1e-72			108.10	CALCIUM/CALMODULIN N-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	
1538	1apm	E	1	270	7e-66			70.09	TRANSHYDROLYSIS OF (AMF)-DEPENDENT PROTEIN KINASE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1538	1b18	A	10	243	14e-34			62.31	(E.C.2.7.1.37) (SC/ARKS) LAPM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 LAPM 4 REPLACED BY ALA (S139AS) COMPLEX WITH THE PEPTIDE LAPM 3 INHIBITOR PKI(5-26) AND THE DETERGENT MEGA-8 LAPM 6	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE; CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN; CDK; INK4; CELL CYCLE COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1538	1b1x	A	1	251	4.2e-37			58.85	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN; CYCLIN-DEPENDENT KINASE; CELL CYCLE 2 CONTROL; ALPHA/BETA; COMPLEX (INHIBITOR PROTEIN/KINASE)
1538	1em8	A	1	270	7e-41			64.67	PHOSPHORYLATED MAP KINASE P38-GAMMA; CHAIN: A, B;	TRANSFERASE STRESS-ACTIVATED PROTEIN KINASE-3; ERK5; ERK5; P38-GAMMA; GAMMA; PHOSPHORYLATION; MAP KINASE
1538	1emk	F	1	270	7e-67			65.16	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pa Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1538	1clp	E	1	270	2.8e-67			74.46	CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	
									TRANSFERRASE/PHOSPHOTRANSFERRASE-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPO) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	
1538	1clx	A	1	257	1.1e-45			75.76	CYCCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: A;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, CELL DIVISION, 2 MITOSIS, INHIBITION
1538	1clm	C	2	262	9.8e-45			75.17	SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A; B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C; D;	TRANSFERRASE KINASE DOMAIN, AUTONHIBITORY FRAGMENT, HOMODIMER
1538	1lgr	A	1	244	4.2e-21			50.75	HGF RECEPTOR I; CHAIN: A; B;	PHOSPHOTRANSFERRASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR I; TRANSFERRASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2
1538	1lct	A	1	270	1.4e-63			87.56	CAMP-DEPENDENT PROTEIN KINASE TYPE I; CHAIN: A;	PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERRASE
									TRANSFERRASE TPRI DELTA; CAMP-DEPENDENT PROTEIN KINASE, OPEN CONFORMATION, PROTEIN 2 KINASE	
1538	1lcl	I	1	257	2.8e-46			66.51	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERRASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEOFOL D score	Compound	PDB annotation
1538	1hw	A	1	270	8.4e-29			57.03	SERINE/THREONINE-PROTEIN KINASE YMAR21G; CHAIN: A;	CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1538	1h8	A	1	253	4.2e-45			82.74	CHK1 CHECKPOINT KINASE; CHAIN: A;	TRANSFERASE PROTEIN KINASE
1538	1lep	A	1	253	2.8e-23			60.07	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A; B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1538	1kbb	A	1	267	7e-65			75.19	TWITCHIN; CHAIN: A; B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1538	1p38	A	1	270	1.4e-40			53.04	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1538	1pkh	A	1	173	1.4e-59			55.11	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1538	1pkh	A	1	246	9.8e-66			107.34	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1538	1pme	A	1	270	1.4e-40			81.42	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Ps Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1538	1qpc	A	1	244	1.3e-21			57.16	LOK KINASE; CHAIN: A;	KINASE, TRANSFERASE
1538	1tdi	A	5	269	9.8e-57			79.61	TITIN; CHAIN: A, B;	TRANSFERASE ALPHA, BETA ROLD
1538	3eik		1	266	1.4e-40			70.45	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TITIN, MUSCLE AUTONINIBITION
1540	1aih	A	725	752	0.0024	-0.24	0.86		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION; OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2, TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1540	1ap2		725	752	0.00024	0.25	0.71		SPIF2; CHAIN: NULL;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1540	1a6	A	725	764	0.006	0.14	0.17		TITIL; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	ZINC FINGER TRANSCRIPTION FACTOR SPI, ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI
1540	1ahd	C	725	752	0.0084	-0.07	0.96		YY1; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX TRANSCRIPTION REGULATORY YING-YANG 1; TRANSCRIPTION INITIATION; INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1540	2gi1	A	725	752	0.0084	0.19	0.59		ZINC FINGER PROTEIN GIL1; CHAIN: A; DNA; CHAIN: C, D;	REGULATION(DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) HYPERFINGER GIL1 ZINC FINGER COMPLEX (DNA-BINDING PROTEIN/DNA)
1542	1apo		911	952	2.4e-15	0.41	0.75		COAGULATION FACTOR EGF-LIKE MODULE OF BLOOD COAGULATION FACTOR X (N-TERMINAL, IAP0 3 APO FORM) (NMR, 13 STRUCTURES) IAP0 4	
1542	1aut	L	915	1050	1.2e-19	0.12	-0.05		ACTIVATED PROTEIN C; CHAIN: C, L; D-PEB-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION(INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION(INHIBITOR) BLOOD COAGULATION BLOOD COAGULATION, EGF, HYDROLASE, SERINE PROTEINASE
1542	1b09		913	948	2.4e-15	0.58	1.00		FACTOR VII; CHAIN: NULL;	
1542	1b10		913	1050	8.4e-27	0.16	-0.17		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE HYDROLASE, PHOSPHOLIPASE A2, PLATELET AGGREGATION INHIBITOR, 2
1542	1dan	L	1018	1108	4.8e-18	0.19	0.03		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; E-SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DPPROMCK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEINASE/COFACTOR/LIGAND)



Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	1st Blast	Verify score	PMF score	SFQ/ROL D score	Compound	PDB annotation
1542	1dan	L	913	1057	1.1e-22	0.18	0.53		BLOOD COAGULATION FACTOR VIIA; CHAIN: L <sub>1</sub> ; H <sub>1</sub> SOLUBLE TISSUE FACTOR; CHAIN: T, U, D-PHE-PHE-ARG-CHLOROMETHYL KETO NE (DPRCKAK) WITH CHAIN: G <sub>1</sub>	BLOOD COAGULATION, SERINE PROTEINASE, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEINASE/COFACTOR(LIGAND))
1542	1ddp	A	913	1049	1.2e-15	0.13	-0.18		THROMBOMODULIN; CHAIN: A <sub>1</sub>	MEMBRANE PROTEIN (NMN, THROMBIN, BGF MODULE, ANTI COAGULANT, GLYCOSYLATION)
1542	1ddp	A	998	1095	3.6e-17	0.58	0.09		THROMBOMODULIN; CHAIN: A <sub>1</sub>	MEMBRANE PROTEIN (NMN, THROMBIN, BGF MODULE, ANTI COAGULANT, GLYCOSYLATION)
1542	1dva	L	913	1057	6e-23	0.13	0.18		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H <sub>1</sub> ; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L <sub>1</sub> ; M <sub>1</sub> (DPR)-PHE-ARG; CHAIN: C <sub>1</sub> ; D <sub>1</sub> PEPTIDE E-76; CHAIN: X <sub>1</sub> ; Y <sub>1</sub>	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1542	1dk5	I	913	1044	3.6e-26	0.21	0.15		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: L <sub>1</sub> , K <sub>1</sub> , L <sub>1</sub> ; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM <sub>1</sub> ; CHAIN: E, F, G, H; FACTOR IX; CHAIN: B, C <sub>1</sub>	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; BGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTI COAGULANT COMPLEX 2 ANTIHEMOLYTIC COMPLEX
1542	1edn	B	913	948	9.6e-14	0.94	1.00		COAGULATION FACTOR CRYSTAL STRUCTURE.	COAGULATION FACTOR CRYSTAL STRUCTURE.

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Pa Blast	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
1542	legf		913	950	2.4e-13	0.85	0.95		GROWTH FACTOR EPIDERMAL GROWTH FACTOR (EGF) (NMAR, 16 STRUCTURES) IEGF 3	EPIDERMAL GROWTH FACTOR, EGF 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
1542	lemn		998	1066	4.8e-19	0.16	0.84		FIBRILLIN, CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1542	legg	A	913	1099	8.4e-25	0.06	-0.13		PROSTAGLANDIN H2 SYNTHASE-I; CHAIN: A, B;	OXIDOREDUCTASE COX-1; EGF DOMAIN, NSAID BINDING, IBUPROFEN, MEMBRANE-BINDING 2 DOMAIN, CYCLOOXYGENASE, PEROXIDASE, OXIDOREDUCTASE, 3
1542	lert	A	920	1108	1.2e-26	0.57	0.24		TUMOR NECROSIS FACTOR RECEPTOR, CHAIN: A, B;	DIOXYGENASE, PEROXIDASE SIGNALING PROTEIN, BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
1542	l76c	A	913	949	7.2e-14	1.02	1.00		BLOOD COAGULATION FACTOR VII, CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING
1542	lhtk	L	913	1057	6e-23	0.19	0.59		BLOOD COAGULATION FACTOR VIIA, CHAIN: L; BLOOD COAGULATION FACTOR VIIA, CHAIN: H;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COAGULANT), BLOOD COAGULATION, 2 SERINE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T.AA	END .AA	Pa Blast	Verify score	PMF score	SEQ/OL D score	Compound	PDB annotation
1542	1ak	L	998	1099	12e-16	-0.00	0.01		SOLUBLE TISSUE FACTOR, CHAIN: T; 5L15; CHAIN: I;	PROTEINASE, COMPLEX, CO-INHIBITOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEINASE/COFACTOR/LIGAND), BLOOD CLOTTING
1542	1ak	L	998	1099	12e-16	-0.00	0.01		BLOOD COAGULATION FACTOR VIA; CHAIN: L; BLOOD COAGULATION FACTOR VIA; CHAIN: H; SOLUBLE TISSUE FACTOR, CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING
1542	18b		916	952	2.4e-15	0.83	0.87		P-SELECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN EGF-LIKE DOMAIN, CELL ADHESION PROTEIN TRANSMEMBRANE, 2 GLYCOPROTEIN
1542	1g44	B	910	1057	3.6e-16	-0.00	-0.18		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1542	1h7	A	1002	1080	2.4e-19	0.34	0.70		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
1542	1h7	A	915	1045	4.8e-20	0.24	0.10		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
1542	1ig	A	913	1082	3.6e-18	0.03	-0.17		INSULIN-LIKE GROWTH FACTOR RECEPTOR I;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR